GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 8, 2003, 18:08:33 ; Search time 2979 Seconds
(without alignments)
11253.661 Million cell updates/sec

Title: US-09-869-414A-3
Perfect score: 2070
Sequence: 1 atggcccaagccctgccctg.....aaaaaaaaaaaaaaaaaaaa 2070

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

:al number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1559.6	75.3	3859	11	AK014464	AK014464 Mus muscu
	2	991.6	47.9	1114	9	AF150387	AF150387 AF150387
	3	958.2	46.3	2503	11	AK014390	AK014390 Mus muscu
	4	819.6	39.6	913	14	BQ949536	BQ949536 AGENCOURT
c	5	746	36.0	747	14	BQ018588	BQ018588 UI-H-DH1-
	6	740.6	35.8	1059	13	BI084083	BI084083 602869445
c	7	723.8	35.0	865	13	BI084878	BI084878 602869445
	8	713.8	34.5	761	13	BM016288	BM016288 603642760
	9	690.2	33.3	904	10	BE378929	BE378929 601237528
c	10	688.6	33.3	700	9	AL570757	AL570757 AL570757
c	11	681.4	32.9	718	12	BF057767	BF057767 7k53e11.x
	12	675.6	32.6	945	14	BQ669630	BQ669630 AGENCOURT
	13	657.8	31.8	684	12	BF338951	BF338951 602036021
	14	644.2	31.1	730	13	BM048418	BM048418 603625683
	15	633	30.6	789	12	BF204338	BF204338 601866411
	16	631	30.5	840	12	BE885725	BE885725 601508937
	17	624	30.1	635	10	BE296749	BE296749 601175134
	18	597	28.8	684	10	AV725513	AV725513 AV725513
	19	595	28.7	623	13	BI828125	BI828125 603075385
	20	591.6	28.6	862	13	BI157614	BI157614 602922587
	21	587.6	28.4	644	12	BE783981	BE783981 601472451
	22	575.8	27.8	720	12	BG288435	BG288435 602383404
c	23	574.2	27.7	649	12	BE837592	BE837592 RC2-FN009
	24	558	27.0	939	12	BF203806	BF203806 601868788
c	25	525	25.4	525	9	AI005033	AI005033 ou91b12.x
c	26	515.2	24.9	541	10	AW770546	AW770546 h186c06.x
	27	511.4	24.7	513	14	BQ637035	BQ637035 he04g12.y
	28	508	24.5	864	12	BE872035	BE872035 601448124
c	29	486.2	23.5	514	12	BF439471	BF439471 nab65a03.
	30	477.8	23.1	605	12	BE793449	BE793449 601588510
	31	472	22.8	487	13	BM313609	BM313609 ig72h03.y
c	32	464	22.4	464	9	AA701598	AA701598 zi34h07.s
c	33	464	22.4	464	9	AI127789	AI127789 qc32c02.x
	34	453.2	21.9	458	9	AL700814	AL700814 DKFZp686H
	35	448	21.6	542	10	AV667139	AV667139 AV667139
	36	447.4	21.6	537	13	BG927600	BG927600 HNC43-1-E
	37	445	21.5	461	9	AL700831	AL700831 DKFZp686I
c	38	444	21.4	444	9	AI095556	AI095556 qb19f04.x
c	39	443	21.4	443	9	AI127822	AI127822 qc36f02.x
	40	441.8	21.3	493	12	BF443234	BF443234 260654 MA
c	41	440.6	21.3	447	10	AW015855	AW015855 UI-H-BI0-
c	42	435.8	21.1	1092	13	BM454007	BM454007 AGENCOURT
c	43	426.4	20.6	428	9	AI094243	AI094243 qa43c11.s
	44	425.8	20.6	573	12	BE799078	BE799078 601588381
c	45	421.8	20.4	425	9	AI857994	AI857994 wj69a09.x

ALIGNMENTS

RESULT 1
AK014464
LOCUS AK014464 3859 bp mRNA linear HTC 19-JAN-2002
DEFINITION Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:4122401C04:beta-site APP cleaving enzyme, full insert sequence.
ACCESSION AK014464
VERSION AK014464.1 GI:12852334
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (strain:C57BL/6J) 16 days embryo head cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:4122401C04.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159

REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851
REFERENCE 5 (bases 1 to 3859)
AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F., Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. cDNA of size comprised between 3 and 7 kb was selected before cloning. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.

FEATURES Location/Qualifiers
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/strain="C57BL/6J"
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/db_xref="MGD:MGI:1896726"
/db_xref="taxon:10090"
/clone="4122401C04"
/tissue_type="head"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="16 days embryo"
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CDS 430. .1935
/gene="Bace"
/note="beta-site APP cleaving enzyme
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AAITESDKFFINGSNWEGILGLAYAEIARPDDSLEPFFDSLVKQTHIPNIFSLQLCGA
GFPLNQTEALASVGGSMIIGGIDHSLYTGSLWYTPIRREWYYEVIIVRVEINGQDLKM
DCKEYNYDKSIVDSGTTNLRLPKKVFEAAVKSIKAASSTEKFPDGFWLGEQLVCWQAG
TTPWNIFPVISLYLMGEVTNQSFRITILPQQYLRPVEDVATSQDDCYKFAVSQSSTGT
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BASE COUNT 873 a 1082 c 1028 g 876 t .
ORIGIN

Query Match 75.3%; Score 1559.6; DB 11; Length 3859;
Best Local Similarity 87.5%; Pred. No. 2.1e-238;
Matches 1798; Conservative 0; Mismatches 244; Indels 12; Gaps 8;

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Db        430 ATGGCCCCAGCGCTGCACTGGCTCCTGCTATGGGTGGGCTCGGGAATGCTGCCTGCCCAG 489

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
              || ||||| | ||||||||||||||||||| |||||||||||||  ||  | ||||||||
Db        490 GGAACCCATCTCGGCATCCGGCTGCCCCTTCGCAGCGGCCTGGCAGGGCCACCCCTGGGC 549

Qy        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
              ||| |||||||||||||||||||||| ||  | |||||||| |||||||| |||||||||
Db        550 CTGAGGCTGCCCCGGGAGACCGACGAGGAATCGGAGGAGCCTGGCCGGAGAGGCAGCTTT 609

Qy        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
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Db        610 GTGGAGATGGTGGACAACCTGAGGGGAAAGTCCGGCCAGGGCTACTATGTGGAGATGACC 669

Qy        241 GTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
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Db        670 GTAGGCAGCCCCCCACAGACGCTCAACATCCTGGTGGACACGGGCAGTAGTAACTTTGCA 729

Qy        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
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Db        730 GTGGGGGCTGCCCCACACCCTTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 789

Qy        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
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Db        790 TATCGAGACCTCCGAAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAGGGGGAA 849

Qy        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
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Qy       481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
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Qy       541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
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Qy       841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
Db      1270 TACAACTACGACAAGAGCATTGTGGACAGTGGGACCACCAACCTTCGCTTGCCCAAGAAA 1329

Qy       901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
Db      1330 GTATTTGAAGCTGCCGTCAAGTCCATCAAGGCAGCCTCCTCGACGGAGAAGTTCCCGGAT 1389

Qy       961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
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Qy      1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
Db      1450 TTCCCAGTCATTTCACTTTACCTCATGGGTGAAGTCACCAATCAGTCCTTCCGCATCACC 1509

Qy      1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
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Db      1570 TACAAGTTCGCTGTCTCACAGTCATCCACGGGCACTGTTATGGGAGCCGTCATCATGGAA 1629

        1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
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Qy      1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320
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Db      1750 GAAGACTGTGGCTACAACATTCCCCAGACAGATGAGTCAACACTTATGACCATAGCCTAT 1809

Qy      1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440
Db      1810 GTCATGGCGGCCATCTGCGCCCTCTTCATGTTGCCACTCTGCCTCATGGTATGTCAGTGG 1869

Qy      1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
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Qy      1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
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Qy      1561 CTTTGGTCACA--AGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCT 1618
Db      1990 CTTTGGTCACATGAGTTGGAGCTATGGATGGTACCTGTGGCCAGAGCACCTCAGGACCCT 2049

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Qy      1739 CTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAAC 1798
Db      2169 TCCTTAGACACCACAAACTTGAGT-TGGAAATTTTGCTGCTTGAAGCTTCAGCCCTGACC 2227

Qy      1799 CTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAG 1858
Db      2228 CTCTGCCCCAGCGTCCTTTAGAGTCTCCAACCTAAAGTATTCTTTATGTC---CTTCCAG 2284

Qy      1859 AAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGA 1918
Db      2285 AAGTACTGGCGTCATACTCAGGCTACC-CGGCATGTGTCCCTGTGGTACCCTGGCAGAGA 2343

Qy      1919 AGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTA 1978
Db      2344 AAGGGCCAATC-TCATTCCCTGCTGGCCAAAGTCAGCAGAAGA--AAGTGAAGTTTGCCA 2400

Qy      1979 TTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT 2038
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Qy      2039 GAATTAAAAAAAAA 2052
Db      2460 GAGATAAACAAGAA 2473
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RESULT 2
AF150387
LOCUS       AF150387               1114 bp    mRNA    linear   EST 22-JUN-1999
DEFINITION  AF150387 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone
            CBMAPH03, mRNA sequence.
ACCESSION   AF150387
VERSION     AF150387.1  GI:5133823
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1114)
  AUTHORS   Ye,M., Zhang,Q.H., Zhou,J., Shen,Y., Wu,X.Y., Guan,Z.Q., Wang,L.,
            Fan,H.Y., Mao,Y.F., Dai,M., Huang,Q.H., Chen,S.J. and Chen,Z.
  TITLE     Human mRNA from cd34+ stem cells
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Ye M
            Shanghai Institute of Hematology
            Shanghai Second Medical University, Rui-Jin Hospital
            197 Rui-Jin Road II, Shanghai, 200025, P. R. China
            Email: zchen@stn.sh.cn.
FEATURES             Location/Qualifiers
     source          1. .1114
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                     /clone="CBMAPH03"
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                     /cell_type="cd34+ stem cell"
                     /note="cloned by differential display method after
                     chemical induction of terminal differentiation of cell
                     line"
BASE COUNT      275 a    300 c    286 g    253 t
ORIGIN

  Query Match             47.9%;  Score 991.6;  DB 9;  Length 1114;
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 Best Local Similarity   97.4%;  Pred. No. 4.6e-148;
 Matches 1093;  Conservative    0;  Mismatches   19;  Indels   10;  Gaps    8;

Qy       712 GGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAG 771
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Db         1 GGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAG 60

Qy       772 TGGTATTATGAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGAC 831
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Qy      1012 TGGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTC 1071
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Db       301 TGGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTC 360

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Db       420 GACGACTGTTAC-AGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTT 478

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Db       479 ATCATGGAGGGCTTCTACCGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTGCTTGT 538

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Qy      1311 CTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGAC 1370
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Db      1013 GCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGAAAATTCTGCTGCTTGAAACTTCA 1072

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RESULT 3
AK014390

LOCUS	AK014390 2503 bp mRNA linear HTC 19-JAN-2002
DEFINITION	Mus musculus adult male brain cDNA, RIKEN full-length enriched library, clone:3526402A15:beta-site APP cleaving enzyme, full insert sequence.
ACCESSION	AK014390
VERSION	AK014390.1 GI:12852207
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (strain:C57BL/6J) adult male brain cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:3526402A15.
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1
AUTHORS	Carninci,P. and Hayashizaki,Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636
REFERENCE	2
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	20499374
PUBMED	11042159
REFERENCE	3
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBMED	11076861
REFERENCE	4
AUTHORS	Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409 (6821), 685-690 (2001)
MEDLINE	21085660
PUBMED	11217851

REFERENCE 5 (bases 1 to 2503)
AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F., Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.
FEATURES Location/Qualifiers

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	/db_xref="MGD:MGI:1896729"
	/db_xref="taxon:10090"
	/clone="3526402A15"
	/sex="male"
	/tissue_type="brain"
	/clone_lib="RIKEN full-length enriched mouse cDNA library"
	/dev_stage="adult"
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polyA_site	2503
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BASE COUNT 615 a 637 c 630 g 621 t

ORIGIN

Query Match 46.3%; Score 958.2; DB 11; Length 2503;
Best Local Similarity 86.2%; Pred. No. 6.2e-143;
Matches 1165; Conservative 0; Mismatches 173; Indels 13; Gaps 9;

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Db          1 TAATCATTGGTGGTATCGACCACTCGCTATACACGGGCAGTCTCTGGTACACACCCATCC 60

Qy        764 GGCGGGAGTGGTATTATGAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGA 823
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Qy        824 AAATGGACTGCAAGGAGTACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACC 883
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Db        121 AGATGGACTGCAAGGAGTACAACTACGACAAGAGCATTGTGGACAGTGGGACCACCAACC 180

Qy        884 TTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCA 943
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Db        181 TTCGCTTGCCCAAGAAAGTATTTGAAGCTGCCGTCAAGTCCATCAAGGCAGCCTCCTCGA 240

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Db        901 GAGCACCTCAGGACCCTCACCAACCTGCCAATGCTTCTGGCGTGACAGA-ACAGAGAAAT 959

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RESULT 4
BQ949536

LOCUS	BQ949536 913 bp mRNA linear EST 21-AUG-2002
DEFINITION	AGENCOURT_8733256 NIH_MGC_101 Homo sapiens cDNA clone IMAGE:6454803 5', mRNA sequence.
ACCESSION	BQ949536
VERSION	BQ949536.1 GI:22365014
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 913)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM2632 row: h column: 04 High quality sequence stop: 613.

FEATURES	Location/Qualifiers
source	1. .913 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:6454803" /clone_lib="NIH_MGC_101" /tissue_type="epidermoid carcinoma, cell line" /lab_host="DH10B (phage-resistant)" /note="Organ: lung; Vector: pOTB7; Site_1: EcoRI; Site_2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 207 a 259 c 232 g 206 t 9 others
ORIGIN

Query Match 39.6%; Score 819.6; DB 14; Length 913;
Best Local Similarity 96.8%; Pred. No. 9.6e-121;
Matches 864; Conservative 0; Mismatches 26; Indels 3; Gaps 3;

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Db         301 TTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGCCAT 360

Qy       1264 GTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATGGAA 1323
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 GTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATGGAA 420

Qy       1324 GACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTATGTC 1383
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 GACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTATGTC 480

Qy       1384 ATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGGCGC 1443
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 ATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGGCGC 540

Qy       1444 TGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTGAAG 1503
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 TGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTGAAG 600

Qy       1504 TGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCACTT 1563
              |||||| ||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db         601 TGAGGANGCCCATGNGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCACTT 660

Qy       1564 TGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCCCCA 1623
              |||||||||||||||||||||||||||||    | ||||||||||||||||||||||||
Db         661 TGGTCACAAGTAGGAGACACAGATGGCACCCTGTGGCAGAGCACCTCAGGACCCTCCCCA 720

Qy       1624 CCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCA-GGG 1682
              |||||||||||||||||||||||||||||||||| |||||||||||| |||||| |||
Db         721 CCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAAGCTGGCAAGGTGNGTTCCAGGGG 780

Qy       1683 ACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACTC- 1741
              |||||||     | |||   |      ||||||||||||||||||||||||||||||
Db         781 ACTGTACCCTGTAGGAACNNGANNAGAGAGAAAGAAGCACTCTGCTGGCGGGAATACTCN 840

Qy       1742 TTGGTCACCTCAAATTTAAGTCGGGAAATTCT-GCTGCTTGAAACTTCAGCCC 1793
              |||||||||||||||||||||||||||||||| |||||||||||| ||| ||
Db         841 TTGGTCACCTCAAATTTAAGTCGGGAAATTCTGGCTGCTTGAAACTCCAGGCC 893
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RESULT 5
BQ018588/c

LOCUS	BQ018588 747 bp mRNA linear EST 27-MAR-2002
DEFINITION	UI-H-DH1-awu-c-12-0-UI.s1 NCI_CGAP_DH1 Homo sapiens cDNA clone IMAGE:5823683 3', mRNA sequence.
ACCESSION	BQ018588
VERSION	BQ018588.1 GI:19753865
KEYWORDS	EST.
SOURCE	human.

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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 747)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jose Mercuende
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
             The following repetitive elements were found in this cDNA
            sequence: 1-22, >AT_rich#Low_complexity
            Seq primer: M13 FORWARD
            POLYA=Yes.
  ATURES              Location/Qualifiers
     source           1. .747
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:5823683"
                      /clone_lib="NCI_CGAP_DH1"
                      /tissue_type="Metastatic Chondrosarcoma"
                      /dev_stage="Adult"
                      /lab_host="DH10B (Life Technologies)"
                      /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                      modified polylinker; Site_1: EcoR I; Site_2: Not I;
                      NCI_CGAP_DH1 is a normalized cDNA library containing the
                      following tissue(s): VS-8 Cell line from Metastatic
                      Chondrosarcoma in Lung. The library was constructed
                      according to Bonaldo, Lennon and Soares, Genome Research,
                      6:791-806, 1996. First strand cDNA synthesis was primed
                      with an oligo-dT primer containing a Not I site. Double
                      stranded cDNA was ligated to an EcoR I adaptor, digested
                      with Not I, and cloned directionally into pT7T3-Pac
                      vector. The oligonucleotide used to prime the synthesis of
                      first-strand cDNA contains a library tag sequence that is
                      located between the Not I site and the (dT)18 tail. The
                      sequence tag for this library is AGATCATTGC.
                      TAG_LIB=UI-H-DH1
                      TAG_TISSUE=lung
                      TAG_SEQ=AGATCATTGC"
BASE COUNT      176 a    178 c    192 g    200 t      1 others
ORIGIN

  Query Match             36.0%;  Score 746;  DB 14;  Length 747;
  Best Local Similarity   99.9%;  Pred. No. 5e-109;
  Matches  746;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1315 GACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATA 1374
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATA 688

Qy       1375 GCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGT 1434
             || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 GCNTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGT 628

Qy       1435 CAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCC 1494
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 CAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCC 568

Qy       1495 CTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGT 1554
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 CTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGT 508

Qy       1555 GGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGA 1614
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGA 448

Qy       1615 CCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGG 1674
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 CCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGG 388

Qy       1675 TTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGG 1734
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 TTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGG 328

Qy       1735 AATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCT 1794
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 AATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCT 268

Qy       1795 GAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTT 1854
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 GAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTT 208

Qy       1855 TCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCA 1914
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 TCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCA 148

Qy       1915 GAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTT 1974
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 GAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTT 88

Qy       1975 GCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCC 2034
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          87 GCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCC 28

Qy       2035 TCTTGAATTAAAAAAAAAAAAAAAAAA 2061
             ||||||||||||||||||||||||||||
Db          27 TCTTGAATTAAAAAAAAAAAAAAAAAA 1


RESULT 6
BI084083
LOCUS       BI084083                1059 bp    mRNA    linear   EST 20-JUN-2001
DEFINITION  602869445F1 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:5013994 5',
            mRNA sequence.
ACCESSION   BI084083
VERSION     BI084083.1  GI:14502413
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1059)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: CLONETECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1820  row: j  column: 11
            High quality sequence stop: 794.
FEATURES              Location/Qualifiers
     source           1. .1059
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:5013994"
                      /clone_lib="NIH_MGC_102"
                      /tissue_type="epidermoid carcinoma, cell line"
                      /lab_host="DH10B (phage-resistant)"
                      /note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
                      Site_2: EcoRI; cDNA made by oligo-dT priming.
                      Directionally cloned into EcoRI/XhoI sites using the
                      following 5' adaptor: GGCACGAG(G).  Library constructed
                      by Ling Hong in the laboratory of Gerald M. Rubin
```

(University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 243 a 300 c 273 g 243 t
ORIGIN

Query Match 35.8%; Score 740.6; DB 13; Length 1059;
Best Local Similarity 92.5%; Pred. No. 3e-108;
Matches 837; Conservative 0; Mismatches 54; Indels 14; Gaps 5;

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Qy        852 CAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAAGTGTTTGAAGC 911
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 CAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAAGTGTTTGAAGC 61

Qy        912 TGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGATGGTTTCTGGCT 971
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGATGGTTTCTGGCT 121

Qy        972 AGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATTTTCCCAGTCAT 1031
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 AGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATTTTCCCAGTCAT 181

Qy       1032 CTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACCATCCTTCCGCA 1091
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACCATCCTTCCGCA 241

Qy       1092 GCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGTTACAAGTTTGC 1151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 GCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGTTACAAGTTTGC 301

Qy       1152 CATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAGGGCTTCTACGT 1211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 CATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAGGGCTTCTACGT 361

Qy       1212 TGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGCCATGTGCACGA 1271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGCCATGTGCACGA 421

Qy       1272 TGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATGGAAGACTGTGG 1331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 TGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATGGAAGACTGTGG 481

Qy       1332 CTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTATGTCATGGCTGC 1391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 CTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTATGTCATGGCTGC 541

Qy       1392 CATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGGCGCTGCCTCCG 1451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 CATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGGCGCTGCCTCCG 601

Qy       1452 CTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTGAAGTGAGGAGG 1511
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Db        602 CTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTGAAGTGAGGAGG 661

Qy       1512 CCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCACTTTGGTCACA 1571
              |||||||||||||||||||||||||  |  |||  |  |    |  || |  ||
Db        662 CCCATGGGCAGAAGATAGAGATTCCCTGGACACACCTCCGTGGTTCACTTTTGGTCACCA 721

Qy       1572 AGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCCCCACCCACCAA 1631
              |||||||||||||||||||||||||||||||||||||||||||  ||  |  ||  ||| |||
Db        722 AGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGAAC---CTCCCACCAACAA 778

Qy       1632 ATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAGGGACTGTACCT 1691
              |||||||||  |||||||||||  | | |||||||||  |  | |  |  ||||||||||
Db        779 ATGCCTCTG-CTTGATGGAGACCG-ACAGGCTGGCACGTGGGTTCC---GGACTGTACCT 833

Qy       1692 GTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACTCTTGGTCACCT 1751
              |||  |||   ||      |  |||||||  |        ||||||||||||||||||||
Db        834 GTACGAACACGA------AGCAAAGAAGAAGCTCCTGTGCGGGAATACTCTTGGTCACTC 887

Qy       1752 CAAAT 1756
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Db        888 AAATT 892
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RESULT 7
BI084878/c
LOCUS BI084878 865 bp mRNA linear EST 20-JUN-2001
DEFINITION 602869445T1 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:5013994 3', mRNA sequence.
ACCESSION BI084878
VERSION BI084878.1 GI:14503208
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 865)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1820 row: j column: 11
High quality sequence start: 18
High quality sequence stop: 821.

FEATURES Location/Qualifiers
source 1. .865
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5013994"
/clone_lib="NIH_MGC_102"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 207 a 224 c 228 g 205 t 1 others
ORIGIN

Query Match 35.0%; Score 723.8; DB 13; Length 865;
Best Local Similarity 95.3%; Pred. No. 1.5e-105;
Matches 810; Conservative 0; Mismatches 33; Indels 7; Gaps 6;

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Qy       1108 GTGGAAGATGTGGCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCC 1167
              ||||||||||| |    || |  |||||||||| || ||||||||||||||||||||
Db         865 GTGGAAGATGTGCCACGTCCCAAGAACGACTGTTAC-AGGTTGCCATCTCACAGTCATCC 807

Qy       1168 ACGGGCACTGTTATGGGAG-CTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGC 1226
              ||||  ||||||||||||| ||||||||||| ||  |    |  ||||||||||
Db         806 ACGGCAACTGTTATGGGAGCCTGTTATCATGGGAGGGCTTCTACGTTGTCTTGATCGGGC 747

Qy       1227 CCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGCCA-TGTGCACGATGAGTTCAGGACGG 1285
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db         746 CCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGCCATTGTGCACGATGAGTTCAGGACGG 687

Qy       1286 CAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATGGAAGACTGTGGC--TACAACATTCC 1343
              |||||||||||||||||||||||| | ||||||||||||||||||      |||||||
Db         686 CAGCGGTGGAAGGCCCTTTTGTCACTTGGGACATGGAAGACTGTGGCATACANACATTCC 627

Qy       1344 ACAGACAGATGAGTCAACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCT 1403
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         626 ACAGACAGATGAGTCAACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCT 567
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Qy       1404 CTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCA 1463
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Db        566 CTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCA 507

Qy       1464 GCAGCATGATGACTTTGCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGA 1523
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        506 GCAGCATGATGACTTTGCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGA 447

Qy       1524 AGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACAC 1583
             |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        446 AGATAGAGATT-CCCTGGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACAC 388

Qy       1584 AGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCT 1643
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 AGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCT 328

Qy       1644 TGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGA 1703
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Db        327 TGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGA 268

             1704 AAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTC 1763
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTC 208

Qy       1764 GGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTC 1823
             |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        207 GGGAAATTCTGCTGCTTGAAACTTCAGGCCTGAACCTTTGTCCACCATTCCTTTAAATTC 148

Qy       1824 TCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTA 1883
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Db        147 TCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTA 88

Qy       1884 CCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTG 1943
             |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db          87 CCTTGGCGTGTGTCCCTGTGGTA-CCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTG 29

Qy       1944 GCCAAAGTCA 1953
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Db          28 GCCAAAGTCA 19
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RESULT 8
BM016288
LOCUS       BM016288                761 bp    mRNA    linear   EST 30-OCT-2001
DEFINITION  603642760F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5418687 5',
            mRNA sequence.
ACCESSION   BM016288
VERSION     BM016288.1  GI:16530642
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 761)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12068  row: h  column: 16
            High quality sequence stop: 728.
FEATURES             Location/Qualifiers
     source          1. .761
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5418687"
                     /clone_lib="NIH_MGC_87"
                     /tissue_type="mammary adenocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 1.383 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
BASE COUNT      170 a    221 c    197 g    171 t      2 others
ORIGIN
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  Query Match             34.5%;  Score 713.8;  DB 13;  Length 761;
  Best Local Similarity   99.3%;  Pred. No. 6.3e-104;
  Matches  726;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy        916 GTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGA 975
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGA 60

Qy        976 GAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATTTTCCCAGTCATCTCA 1035
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATTTTCCCAGTCATCTCA 120

Qy       1036 CTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAA 1095
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAA 180

Qy       1096 TACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGTTACAAGTTTGCCATC 1155
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGTTACAAGTTTGCCATC 240

Qy       1156 TCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTC 1215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||
Db        241 TCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAGGGCTTCTACNGTGTC 300

Qy       1216 TTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAG 1275
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        301 TTTGATCGGGCCCGAAAACGAANTGGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAG 360

Qy       1276 TTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATGGAAGACTGTGGCTAC 1335
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATGGAAGACTGTGGCTAC 420

Qy       1336 AACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTATGTCATGGCTGCCATC 1395
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTATGTCATGGCTGCCATC 480

Qy       1396 TGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGGCGCTGCCTCCGCTGC 1455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGGCGCTGCCTCCGCTGC 540

Qy       1456 CTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCA 1515
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCA 600

Qy       1516 TGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCACTTTGGTCACAAGTA 1575
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Db        601 TGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCACTTTGGTCACAAGTA 660

Qy       1576 GGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCCCCACCCACCAAATGC 1635
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||| ||||||
Db        661 GGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCCCCA-CCACAAAATGC 719

Qy       1636 CTCTGCCTTGA 1646
              ||||||||||||
Db        720 CTCTGCCTTGA 730
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RESULT 9
BE378929
LOCUS       BE378929                904 bp    mRNA    linear   EST 21-JUL-2000
DEFINITION  601237528F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609631 5',
            mRNA sequence.
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ACCESSION   BE378929
VERSION     BE378929.1  GI:9324294
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 904)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM264  row: g  column: 08
            High quality sequence stop: 735.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:3609631"
                     /clone_lib="NIH_MGC_44"
                     /tissue_type="endometrium, adenocarcinoma cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Library constructed  by Ling Hong
                     in the laboratory of Gerald M. Rubin (University of
                     California,  Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life  Technologies)."
BASE COUNT      191 a    240 c    256 g    217 t
ORIGIN

  Query Match             33.3%;  Score 690.2;  DB 10;  Length 904;
  Best Local Similarity   98.1%;  Pred. No. 3.2e-100;
  Matches  741;  Conservative    0;  Mismatches    8;  Indels    6;  Gaps    4;

Qy        749 GGTATACACCCATCCGGCGGGAGTGGTATTATGAGGT-CATCATTGTGCGGGTGGAGATC 807
              ||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db          1 GGTATACACCCATCCGGCGGGAGTGGTATTATGAGGTCCATCATTGTGCGGGTGGAGATC 60

          808 AATGGACAGGATCTGAAAATGGACTGCAAGGAGTACAACTATGACAAGAGCATTGTGGAC 867
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATGGACAGGATCTGAAAATGGACTGCAAGGAGTACAACTATGACAAGAGCATTGTGGAC 120

Qy        868 AGTGGCACCACCAACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATC 927
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGTGGCACCACCAACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATC 180

Qy        928 AA-GGCAGCCTCCTCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGT 986
              || |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        181 AAGGGCAGCCTCCTCCACGGAGAAGTTCCTTGATGGTTTCTGGCTAGGAGAGCAGCTGGT 240

Qy        987 GTGCTGGCAAGCAGGCACCACCCCTTGGAACATTTTCCCAGTCATCTCACTCTACCTAAT 1046
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGCTGGCAAGCAGGCACCACCCCTTGGAACATTTTCCCAGTCATCTCACTCTACCTAAT 300

Qy       1047 GGGTGAGGTTACCAACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCC 1106
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        301 GGGTGAGGTTACCAACCAGTCCTTCCGCATCACCATCCTTCCGTAGCAATACCTGCGGCC 360

Qy       1107 AGTGGAAGATGTGGCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATC 1166
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGTGGAAGATGTGGCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATC 420

Qy       1167 CACGGGCACTGTTATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGC 1226
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CACGGGCACTGTTATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGC 480

Qy       1227 CCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGC 1286
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Db        481 CCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGC 540

Qy       1287 AGCGGTGGAAGGCCCTTTTGTCACCTTGGACATGGAAGACTGTGGCTACAACATTCCACA 1346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCGGTGGAAGGCCCTTTTGTCACCTTGGACATGGAAGACTGTGGCTACAACATTCCACA 600

Qy       1347 GACAGATGAGTCAACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTT 1406
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GACAGATGAGTCAACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTT 660

Qy       1407 CATGCTGCCACTCTGCCTCATGGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCA 1466
              ||||||| |||||||||||||||||||||||||||||||    |  |    ||||||||||
Db        661 CATGCTG-CACTCTGCCTCATGGTGTGTCAGTGGCGCTG---CTCCGTGCTGCGCCAGCA 716

Qy       1467 GCATGATGACTTTGCTGATGACATCTCCCTGCTGA 1501
              ||||||||||||| ||||||||||||||||||||
Db        717 GCATGATGACTTTGGTGATGACATCTCCCTGCTGA 751


RESULT 10
AL570757/c
LOCUS       AL570757                700 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  AL570757 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI022YF22 3
            prime, mRNA sequence.
ACCESSION   AL570757
VERSION     AL570757.1  GI:12927378
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 700)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .700
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DI022YF22"
                     /clone_lib="LTI_NFL006_PL2"
                     /tissue_type="placenta"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer.  Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      169 a    173 c    191 g    161 t      6 others
ORIGIN

  Query Match             33.3%;  Score 688.6;  DB 9;  Length 700;
  Best Local Similarity   99.3%;  Pred. No. 6.5e-100;
  Matches  688;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1250 TCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCA 1309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         693 TCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCA 634

Qy       1310 CCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGA 1369
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              |:||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         633 CYTTGYACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGA 574

Qy        1370 CCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGG 1429
              |||||||||||||||||||||||||| |||||||||| |||||||||||||||||||||||
Db         573 CCATAGCCTATGTCATGGCTGCCATNTGCGCCCTCTTNATGCTGCCACTCTGCCTCATGG 514

Qy        1430 TGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACA 1489
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         513 TGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACA 454

Qy        1490 TCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACC 1549
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         453 TCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACC 394

Qy        1550 TCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCT 1609
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         393 TCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCT 334

Qy        1610 CAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAG 1669
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         333 CAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAG 274

Qy        1670 GTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTG 1729
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         273 GTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTG 214

Qy        1730 GCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCA 1789
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Db         213 GCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCA 154

Qy        1790 GCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCT 1849
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         153 GCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCT 94

Qy        1850 TAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCC 1909
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          93 TAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCC 34

Qy        1910 TGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCT 1942
              |||||||||||||:|||||||||||||||||||
Db          33 TGGCAGAGAAGAGWCCAAGCTTGTTTCCCTGCT 1
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RESULT 11
BF057767/c

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LOCUS       BF057767                718 bp    mRNA    linear   EST 16-OCT-2000
DEFINITION  7k53e11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3479156 3'
            similar to TR:Q9ULS1 Q9ULS1 KIAA1149 PROTEIN ;, mRNA sequence.
ACCESSION   BF057767
VERSION     BF057767.1  GI:10811663
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 718)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            R. Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL, send email to:
            info@image.llnl.gov
            Seq primer: -40UP from Gibco
            High quality sequence stop: 465.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:3479156"
                     /clone_lib="NCI_CGAP_GC6"
                     /tissue_type="pooled germ cell tumors"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
                     from the normalized library NCI_CGAP_GC4 was prepared, and
                     ss circles were made in vitro. Following HAP purification,
                     this DNA was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from a pool
                     of 5,000 clones made from the same library (cloneIDs
                     1257096-1258631, 1469064-1470983, and 1475592-1476743).
                     Subtraction by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      174 a    177 c    190 g    176 t      1 others
ORIGIN
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  Query Match             32.9%;  Score 681.4;  DB 12;  Length 718;
  Best Local Similarity   99.3%;  Pred. No. 8.9e-99;
  Matches  715;  Conservative    0;  Mismatches    2;  Indels    3;  Gaps    3;

Qy        1306 GTCACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTC 1365
               |||||||||||||||||||||||||||| |||||||||||||||||||||||| ||||
Db         718 GTCACCTTGGACATGGAAGACTGTGGCTAC-ACATTCCACAGACAGATGAGTCAA-CCTC 661

Qy        1366 ATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTC 1425
               |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         660 ATGACCATAGCTTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTC 601

Qy        1426 ATGGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGAT 1485
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         600 ATGGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGAT 541

Qy        1486 GACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCA 1545
               |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db         540 GACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCNTGGACCA 481

Qy        1546 CACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGC 1605
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         480 CACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGC 421

Qy        1606 ACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGG 1665
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         420 ACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGG 361

Qy        1666 CAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCT 1725
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         360 CAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCT 301

Qy        1726 GCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAAC 1785
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         300 GCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAAC 241

Qy        1786 TTCAGCCCTGAACC-TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCT 1844
               |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db         240 TTCAGCCCTGAACCTTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCT 181

Qy        1845 TTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGG 1904
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         180 TTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGG 121

Qy        1905 TACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGA 1964
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         120 TACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGA 61

Qy        1965 TGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGC 2024
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          60 TGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGC 1
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RESULT 12
BQ669630
LOCUS       BQ669630                945 bp    mRNA    linear   EST 15-JUL-2002
DEFINITION  AGENCOURT_8354446 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6275949
            5', mRNA sequence.
ACCESSION   BQ669630
VERSION     BQ669630.1  GI:21780464
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 945)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2459  row: o  column: 22
            High quality sequence stop: 506.
FEATURES             Location/Qualifiers
     source          1. .945
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                     /clone="IMAGE:6275949"
                     /clone_lib="NIH_MGC_102"
                     /tissue_type="epidermoid carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G).  Library constructed
                     by Ling Hong in the laboratory of Gerald M. Rubin
                     (University of  California, Berkeley) using ZAP-cDNA
                     synthesis kit (Stratagene) and Superscript II RT (Life
                     Technologies). Note: this is a NIH_MGC Library."
BASE COUNT      253 a    231 c    245 g    214 t      2 others
ORIGIN

  Query Match             32.6%;  Score 675.6;  DB 14;  Length 945;
  Best Local Similarity   99.0%;  Pred. No. 6.5e-98;
  Matches  689;  Conservative    0;  Mismatches    6;  Indels    1;  Gaps    1;

Qy       1365 CATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCT 1424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCT 60

Qy       1425 CATGGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGA 1484
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CATGGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGA 120

Qy       1485 TGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACC 1544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACC 180

Qy       1545 ACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAG 1604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAG 240

Qy       1605 CACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTG 1664
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTG 300

Qy       1665 GCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTC 1724
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        301 GCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTC 360

Qy       1725 TGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAA 1784
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAA 420

Qy       1785 CTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCT 1844
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCT 480

Qy       1845 TTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGG 1904
             ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        481 TTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGGTACCTTGGCGTGTGTCCCTGTGG 540

Qy       1905 TACCCT-GGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGG 1963
             |||||| ||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        541 TACCCTGGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCANAGTCAGTAGGAGAGG 600

Qy       1964 ATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTG 2023
             |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        601 ATGCACAGTTTGCTATTTGCTTTANAGACAGGGACTGTATAAACAAGCCTAACATTGGTG 660

Qy       2024 CAAAGATTGCCTCTTGAATTAAAAAAAAAAAAAAAA 2059
             |||||||||||||||||||||||||||||  | |
Db        661 CAAAGATTGCCTCTTGAATTAAAAAAAAAACTAGA 696


RESULT 13
BF338951
LOCUS       BF338951                684 bp    mRNA    linear   EST 22-NOV-2000
DEFINITION  602036021F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4184140
            5', mRNA sequence.
ACCESSION   BF338951
VERSION     BF338951.1  GI:11285371
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 684)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9501  row: i  column: 05
            High quality sequence stop: 652.
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                     /db_xref="taxon:9606"
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                     /clone_lib="NCI_CGAP_Brn64"
                     /tissue_type="glioblastoma with EGFR amplification"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.57 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      161 a    189 c    172 g    162 t
ORIGIN

  Query Match             31.8%;  Score 657.8;  DB 12;  Length 684;
  Best Local Similarity   99.4%;  Pred. No. 5e-95;
  Matches  681;  Conservative    0;  Mismatches    2;  Indels    2;  Gaps    2;
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Qy       1229 GAAAACGAATTGGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAG 1288
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAAAACGAATTGGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAG 60

Qy       1289 CGGTGGAAGGCCCTTTTGTCACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGA 1348
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGTGGAAGGCCCTTTTGTCACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGA 120

Qy       1349 CAGATGAGTCAACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCA 1408
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGATGAGTCAACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCA 180

Qy       1409 TGCTGCCACTCTGCCTCATGGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGC 1468
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGCTGCCACTCTGCCTCATGGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGC 240

Qy       1469 ATGATGACTTTGCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATA 1528
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Db        241 ATGATGACTTTGCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATA 300

Qy       1529 GAGATTCCCCTGGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATG 1588
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Db        301 GAGATTCCCCTGGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATG 360

Qy       1589 GCACCTGTGGCCAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATG 1648
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCACCTGTGGCCAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATG 420

Qy       1649 GAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGA 1708
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Db        421 GAGAAGGAAAAGGCTGGCAAGGTGGGTTCCA-GGACTGTACCTGTAGGAAACAGAAAAGA 479

Qy       1709 GAAGAAAGAAGCACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAA 1768
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Db        480 GAAGAAAGAAGCACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAA 539

Qy       1769 ATTCTGCTGCTTGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAA 1828
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Db        540 ATTCTGCTGCTTGAAACTTCAGCCCTGAACCTTGGTCCACCATTCCTTTAAATTCTCCAA 599

Qy       1829 CCC-AAAGTATTCTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTT 1887
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Db        600 CCCAAAAGTATTCTTCTTTTCTTAGTTCCAGAAGTACTGGCATCACACGCAGGTTACCTT 659

Qy       1888 GGCGTGTGTCCCTGTGGTACCCTGG 1912
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Db        660 GGCGTGTGTCCCTGTGGTACCCTGG 684
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RESULT 14
BM048418

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LOCUS       BM048418               730 bp    mRNA    linear   EST 07-NOV-2001
DEFINITION  603625683F1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:5452052 5',
            mRNA sequence.
ACCESSION   BM048418
VERSION     BM048418.1  GI:16777685
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 730)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1943  row: f  column: 21
            High quality sequence stop: 696.
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                     /tissue_type="carcinoma, cell line"
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                     /note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Library constructed  by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California,  Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life  Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      163 a    210 c    206 g    151 t
ORIGIN
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Query Match 31.1%; Score 644.2; DB 13; Length 730;
Best Local Similarity 96.7%; Pred. No. 7e-93;
Matches 711; Conservative 0; Mismatches 18; Indels 6; Gaps 5;

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              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GATGACCGTGGGCAG-CCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAA 60

Qy        294 CTTTGCAGTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTC 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTTTGCAGTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTC 120

Qy        354 CAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGA 413
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Db        121 CAGCACATACCGGGA-CTCCGGAAGGGTGTGTATGTGCCCTACACCCA-GGCAAGTGGGA 178

Qy        414 AGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGC 473
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        179 AGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGG-CCCAACGTCACTGTGCGTGC 237

Qy        474 CAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGG 533
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 CAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGG 297

Qy        534 CATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTT 593
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Db        358 TGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGC 417

Qy        654 TGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGG 713
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Qy        714 AGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTG 773
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Qy        774 GTATTATGAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTG 833
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Db        538 GTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGACACTGGACTG 597

Qy        834 CAAGGAGTACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCC 893
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Db        598 CAAGGAGTACAAGTATGACAAGAGCATTGGGGACAGTGGCACCAC--AACCTGCGATGCC 655

Qy        894 CAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTT 953
              |||||||||||  |||||||||||||||||||||||||| || |||||||||||| |
Db        656 CAAGAAAGTGTCGGAAGCTGCAGTCAAATCCATCAAGGCAGCATCGTCCACGGAGAAGGT 715
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Qy        954 CCCTGATGGTTTCTG 968
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Db        716 CCCTGATGGTTACTG 730


RESULT 15
BF204338
LOCUS       BF204338                789 bp    mRNA    linear   EST 06-NOV-2000
DEFINITION  601866411F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4106858 5',
            mRNA sequence.
ACCESSION   BF204338
VERSION     BF204338.1  GI:11097924
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 789)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM987  row: e  column: 03
            High quality sequence stop: 716.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:4106858"
                     /clone_lib="NIH_MGC_17"
                     /tissue_type="rhabdomyosarcoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
                     Site_2: XhoI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G).  Size-selected >500bp
                     for average insert size 1.8kb.  Library constructed by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      180 a    204 c    215 g    190 t
ORIGIN

  Query Match             30.6%;  Score 633;  DB 12;  Length 789;
  Best Local Similarity   99.6%;  Pred. No. 4e-91;
  Matches  666;  Conservative    0;  Mismatches    0;  Indels    3;  Gaps    3;

Qy        778 TATGAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAG 837
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 TATGAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAG 61

Qy        838 GAGTACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG 897
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 GAGTACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG 121

Qy        898 AAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCT 957
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Db        122 AAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCT 181

Qy        958 GATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAAC 1017
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Db        182 GATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCC-TGGAAC 240

Qy       1018 ATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATC 1077
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATC 300

Qy       1078 ACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGAC 1137
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Db        301 ACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGAC 360

Qy       1138 TGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG 1197
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Qy       1258 TGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGAC 1317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGAC 540

Qy       1318 ATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC 1377
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Qy       1438 TGGCGCTGC 1446
              |||||||||
Db        659 TGGCGCTGC 667


Search completed: July  8, 2003, 19:45:54
Job time : 2985 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 9, 2003, 09:54:03 ; Search time 101 Seconds
(without alignments)
6285.355 Million cell updates/sec

Title: US-09-869-414A-3
Perfect score: 2070
Sequence: 1 atggcccaagccctgccctg.....aaaaaaaaaaaaaaaaaaaa 2070

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	2068.4	99.9	2070	4	US-09-548-367D-3	Sequence 3, Appli
3	2032	98.2	2541	4	US-09-009-191-1	Sequence 1, Appli
4	1887.2	91.2	1977	4	US-09-548-372D-5	Sequence 5, Appli
5	1887.2	91.2	1977	4	US-09-548-367D-5	Sequence 5, Appli
6	1843.4	89.1	2370	4	US-09-009-191-3	Sequence 3, Appli
7	1552.4	75.0	2043	4	US-09-548-372D-7	Sequence 7, Appli
8	1552.4	75.0	2043	4	US-09-548-367D-7	Sequence 7, Appli
9	1359	65.7	1362	4	US-09-548-372D-29	Sequence 29, Appl
10	1359	65.7	1362	4	US-09-548-367D-29	Sequence 29, Appl
11	1359	65.7	1380	4	US-09-548-372D-31	Sequence 31, Appl
12	1359	65.7	1380	4	US-09-548-367D-31	Sequence 31, Appl
13	1297	62.7	1341	4	US-09-548-372D-21	Sequence 21, Appl
14	1297	62.7	1341	4	US-09-548-367D-21	Sequence 21, Appl
15	1297	62.7	1380	4	US-09-548-372D-23	Sequence 23, Appl
16	1297	62.7	1380	4	US-09-548-367D-23	Sequence 23, Appl
17	1294.8	62.6	1506	4	US-09-713-158-1	Sequence 1, Appli
18	1273.6	61.5	1302	4	US-09-548-372D-25	Sequence 25, Appl
19	1273.6	61.5	1302	4	US-09-548-367D-25	Sequence 25, Appl
20	1199	57.9	1287	4	US-09-548-372D-50	Sequence 50, Appl
21	1199	57.9	1287	4	US-09-548-367D-50	Sequence 50, Appl
22	1199	57.9	1305	4	US-09-548-372D-52	Sequence 52, Appl
23	1199	57.9	1305	4	US-09-548-367D-52	Sequence 52, Appl
24	1183.2	57.2	1278	4	US-09-548-372D-27	Sequence 27, Appl
25	1183.2	57.2	1278	4	US-09-548-367D-27	Sequence 27, Appl
26	421.2	20.3	511	4	US-09-280-116-30	Sequence 30, Appl
27	393.4	19.0	1545	4	US-09-717-432-1	Sequence 1, Appli
28	393.4	19.0	1545	4	US-09-912-484-1	Sequence 1, Appli
29	393.4	19.0	1804	4	US-09-548-372D-1	Sequence 1, Appli
30	393.4	19.0	1804	4	US-09-548-367D-1	Sequence 1, Appli
31	391.8	18.9	1862	3	US-08-999-723-1	Sequence 1, Appli
32	391.8	18.9	1862	4	US-09-434-427-1	Sequence 1, Appli
33	307	14.8	1021	4	US-09-280-116-85	Sequence 85, Appl
c 34	301.8	14.6	434	4	US-09-280-116-31	Sequence 31, Appl
35	198.8	9.6	2514	4	US-09-280-116-32	Sequence 32, Appl
36	84.4	4.1	306	4	US-09-280-116-52	Sequence 52, Appl
37	64.2	3.1	77	4	US-09-548-372D-39	Sequence 39, Appl
c 38	64.2	3.1	77	4	US-09-548-372D-40	Sequence 40, Appl
39	64.2	3.1	77	4	US-09-548-367D-39	Sequence 39, Appl
c 40	64.2	3.1	77	4	US-09-548-367D-40	Sequence 40, Appl
41	46.8	2.3	393	4	US-09-280-116-34	Sequence 34, Appl
c 42	46.2	2.2	2900	1	US-08-034-650-9	Sequence 9, Appli
c 43	46.2	2.2	2900	1	US-08-449-015-9	Sequence 9, Appli
44	45.8	2.2	30001	1	US-08-125-468-1	Sequence 1, Appli
45	45.8	2.2	30001	2	US-08-474-933-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-548-372D-3
; Sequence 3, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-548-372D-3

Query Match 99.9%; Score 2068.4; DB 4; Length 2070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2069; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120

Qy        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
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Db        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy        241 GTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
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Db        241 GTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
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Qy       301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
Db       301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy       361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
Db       361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy       421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
Db       421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy       481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
Db       481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540

Qy       541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
Db       541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600

Qy       601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
Db       601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGCTTC 660

Qy       661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
Db       661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720

Qy       721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
Db       721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780

Qy       781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
Db       781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840

Qy       841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
Db       841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900

Qy       901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
Db       901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960

Qy       961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
Db       961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020

Qy      1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
Db      1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080

Qy      1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
Db      1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140

Qy      1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
Db      1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200

Qy      1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
Db      1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260

Qy      1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320
Db      1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320

Qy      1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
Db      1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380

Qy      1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440
Db      1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440

Qy      1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
Db      1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500

Qy      1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
Db      1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560

Qy      1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620
Db      1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620

Qy      1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680
Db      1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680

Qy      1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740
Db      1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740

Qy      1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
Db      1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800

Qy      1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
Db      1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860

Qy      1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
Db      1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920

Qy      1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
Db      1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980

Qy      1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
Db      1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040

Qy      2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
Db      2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
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RESULT 2
US-09-548-367D-3
; Sequence 3, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2070
; TYPE: DNA

; ORGANISM: Homo sapiens
US-09-548-367D-3

Query Match 99.9%; Score 2068.4; DB 4; Length 2070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2069; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
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Db          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
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Qy        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
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            181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
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Qy        241 GTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
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Qy        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
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Db        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
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Db        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

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Qy        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
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Db        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900

Qy        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
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Db        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960

Qy        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
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Db        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020

Qy       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
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Qy       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
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Db       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140

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Db       1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560

Qy       1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620
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Db       1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620

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Db       1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680

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Db       1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740

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Qy       1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
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Db       1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860

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Db       1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920

Qy       1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
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Db       1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980

Qy       1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040

Qy       2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
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Db       2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
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RESULT 3
US-09-009-191-1
; Sequence 1, Application US/09009191
; Patent No. 6319689
;  GENERAL INFORMATION:
;    APPLICANT:  POWELL, DAVID
;    APPLICANT:  CHAPMAN, CONRAD
;    APPLICANT:  MURPHY, KAY
;    APPLICANT:  SMITH, TRUDI
;    TITLE OF INVENTION:  ASP2
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RATNER & PRESTIA
;      STREET:  P.O. BOX 980
;      CITY:  VALLEY FORGE
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19482
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/009,191
;      FILING DATE:  20-JAN-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  UK 9701684.4
;      FILING DATE:  28-JAN-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PRESTIA, PAUL F
;      REGISTRATION NUMBER:  23,031
;      REFERENCE/DOCKET NUMBER:  GH-70368
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-407-0700
;      TELEFAX:  610-407-0701
;      TELEX:  846169
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2541 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-009-191-1

  Query Match             98.2%;  Score 2032;  DB 4;  Length 2541;
  Best Local Similarity   99.5%;  Pred. No. 0;
  Matches 2049;  Conservative    0;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120

Qy        121 CTGCGGCTGCCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGCGGCTGCCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300

Qy        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        361 TACCGGGACCTCCGGAAGGGTGTGTATGAGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540

Qy        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
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Db        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600

Qy        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGCTTC 660

Qy        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720

Qy        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780

Qy        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840

Qy        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900

Qy        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960

Qy        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020

Qy       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080

Qy       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140

Qy       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200

Qy       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260

Qy       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320

Qy       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380

Qy       1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440
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Db       1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440

Qy       1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
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Db       1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500

Qy       1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT-GGACCACACCTCCGTGGTTC 1559
             |||||||||||||||||||    |||||||||||||||| ||||||||||||||||||||
Db       1501 AAGTGAGGAGGCCCATGGGAGAAAGATAGAGATTCCCCTGGGACCACACCTCCGTGGTTC 1560

Qy       1560 ACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTC 1619
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTC 1620

Qy       1620 CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCA 1679
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCA 1680

Qy       1680 GGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATAC 1739
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATAC 1740

Qy       1740 TCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACC 1799
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Db       1741 TCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACC 1800

Qy       1800 TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGA 1859
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGA 1860

Qy       1860 AGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAA 1919
             |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db       1861 AGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCGGGCAGAGAA 1920

Qy       1920 GAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTAT 1979
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 GAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTAT 1980

Qy       1980 TTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTG 2039
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 TTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTG 2040

Qy       2040 AATTAAAAAAAAAAAAAAAA 2059
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Db       2041 AATTAAAAAAAAAAACTAGA 2060
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  SULT 4
  -09-548-372D-5
; Sequence 5, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280I
;  CURRENT APPLICATION NUMBER: US/09/548,372D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 1977
;   TYPE: DNA
;   ORGANISM: Homo  sapiens
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US-09-548-372D-5

Query Match 91.2%; Score 1887.2; DB 4; Length 1977;
Best Local Similarity 96.2%; Pred. No. 0;
Matches 1974; Conservative 0; Mismatches 3; Indels 75; Gaps 1;

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Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120

Qy        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy        241 GTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
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Db        241 GTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300

Qy        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540

Qy        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
              |||||||||||||||||||||||||||
Db        541 GGGCTGGCCTATGCTGAGATTGCCAGG---------------------------------- 567

Qy        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
                                                                ||||||||||||||||||
Db        568 ----------------------------------------CTTTGTGGTGCTGGCTTC 585

Qy        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 645

Qy        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 705

Qy        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 765

Qy        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
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Db        766 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 825

Qy        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        826 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 885

Qy        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        886 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 945
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Qy       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
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Db        946 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1005

Qy       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1006 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1065

Qy       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1066 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1125

Qy       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
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Db       1126 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1185

Qy       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320
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Db       1186 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1245

Qy       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
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Db       1246 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1305

Qy       1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1306 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1365

Qy       1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1366 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1425

Qy       1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1426 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1485

Qy       1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1486 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1545

Qy       1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1546 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1605

Qy       1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740
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Db       1606 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1665

Qy       1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
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Db       1666 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCGCTGAACCT 1725

Qy       1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
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Db       1726 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1785

Qy       1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1786 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1845

Qy       1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1846 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1905

Qy       1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1906 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 1965

Qy       2041 ATTAAAAAAAAA 2052
             |  |||||||||
Db       1966 AAAAAAAAAAAA 1977
```

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RESULT 5
US-09-548-367D-5
; Sequence 5, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280H
;  CURRENT APPLICATION NUMBER: US/09/548,367D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 1977
;   TYPE: DNA
;   ORGANISM: Homo  sapiens
US-09-548-367D-5

  Query Match             91.2%;  Score 1887.2;  DB 4;  Length 1977;
  Best Local Similarity   96.2%;  Pred. No. 0;
  Matches 1974;  Conservative    0;  Mismatches    3;  Indels   75;  Gaps    1;

Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGGCGCCCCCCTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120

Qy        121 CTGCGGCTGCCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGCGGCTGCCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy        241 GTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300

Qy        301 GTGGGTGCTGCCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGGGTGCTGCCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540

Qy        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
              |||||||||||||||||||||||||||
Db        541 GGGCTGGCCTATGCTGAGATTGCCAGG---------------------------------- 567

Qy        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
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Db        568 ----------------------------------------CTTTGTGGTGCTGGCTTC 585

Qy        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 645

Qy        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 705

Qy        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 765

Qy        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        766 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 825

Qy        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        826 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 885

Qy        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        886 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 945

Qy       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        946 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1005

Qy       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1006 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1065

Qy       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1066 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1125

Qy       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1126 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1185

Qy       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1186 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1245

Qy       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1246 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1305

Qy       1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1306 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1365

Qy       1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1366 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1425

Qy       1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1426 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1485

Qy       1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1486 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1545

Qy       1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1546 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1605

Qy       1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       1606 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1665

Qy       1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1666 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1725

Qy       1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1726 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1785

Qy       1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1786 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1845

Qy       1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1846 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1905

Qy       1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1906 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 1965

Qy       2041 ATTAAAAAAAAA 2052
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Db       1966 AAAAAAAAAAAA 1977
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RESULT 6
US-09-009-191-3
; Sequence 3, Application US/09009191
; Patent No. 6319689
;  GENERAL INFORMATION:
;    APPLICANT:  POWELL, DAVID
;    APPLICANT:  CHAPMAN, CONRAD
;    APPLICANT:  MURPHY, KAY
;    APPLICANT:  SMITH, TRUDI
;    TITLE OF INVENTION:  ASP2
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RATNER & PRESTIA
;      STREET:  P.O. BOX 980
;      CITY:  VALLEY FORGE
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19482
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/009,191
;      FILING DATE:  20-JAN-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  UK 9701684.4
;      FILING DATE:  28-JAN-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PRESTIA, PAUL F
;      REGISTRATION NUMBER:  23,031
;      REFERENCE/DOCKET NUMBER:  GH-70368
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-407-0700
;      TELEFAX:  610-407-0701
;      TELEX:  846169
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2370 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-009-191-3
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Query Match             89.1%;  Score 1843.4;  DB 4;  Length 2370;
Best Local Similarity   98.8%;  Pred. No. 0;
Matches 1867;  Conservative    0;  Mismatches   21;  Indels    1;  Gaps    1;

Qy        172 GGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTG 231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTG 60

Qy        232 GAGATGACCGTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGT 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAGATGACCGTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGT 120

Qy        292 AACTTTGCAGTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTG 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACTTTGCAGTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTG 180

Qy        352 TCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGG 411
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        181 TCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGAGCCCTACACCCAGGGCAAGTGG 240

Qy        412 GAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGT 471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGT 300

Qy        472 GCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAA 531
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAA 360

Qy        532 GGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTC 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTC 420

Qy        592 TTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGT 651
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGT 480

Qy        652 GCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATT 711
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||.
Db        481 GCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATT 540

Qy        712 GGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAG 771
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAG 600

Qy        772 TGGTATTATGAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGAC 831
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGAC 660

Qy        832 TGCAAGGAGTACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTG 891
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGCAAGGAGTACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTG 720

Qy        892 CCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAG 951
              |||||||||||||||||||||||||||||||||||||||||||||||| | |||||||||
Db        721 CCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCTCCACGGGAGAAG 780

Qy        952 TTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCT 1011
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCT 840

Qy       1012 TGGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTC 1071
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TGGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTC 900

Qy       1072 CGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAA 1131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAA 960

Qy       1132 GACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTT 1191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTT 1020

Qy       1192 ATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTC 1251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 ATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTC 1080

Qy       1252 AGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACC 1311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1081 AGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACC 1140

Qy       1312 TTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACC 1371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1141 TTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACC 1200

Qy       1372 ATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTG 1431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1201 ATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTG 1260

Qy       1432 TGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATC 1491
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        1261 TGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGACAATGGATGACTTTGCTGATGACATC 1320

Qy       1492 TCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT-GGACCACACCT 1550
              |||||||||||||||||||||||||||||||  ||||||||||||||| ||||||||||
Db        1321 TCCCTGCTGAAGTGAGGAGGCCCATGGGAGAAAGATAGAGATTCCCCTGGGACCACACCT 1380

Qy       1551 CCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTC 1610
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1381 CCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTC 1440

Qy       1611 AGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGG 1670
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1441 AGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGG 1500

Qy       1671 TGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGG 1730
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1501 TGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGG 1560

Qy       1731 CGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAG 1790
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1561 CGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAG 1620

Qy       1791 CCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTT 1850
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1621 CCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTT 1680

Qy       1851 AGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCT 1910
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Db        1681 AGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCG 1740

Qy       1911 GGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACA 1970
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1741 GGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACA 1800

Qy       1971 GTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGAT 2030
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1801 GTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGAT 1860

Qy       2031 TGCCTCTTGAATTAAAAAAAAAAAAAAAA 2059
              |||||||||||||||||||||||| | |
Db        1861 TGCCTCTTGAATTAAAAAAAAAAACTAGA 1889
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RESULT 7
US-09-548-372D-7
; Sequence 7, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280I
;  CURRENT APPLICATION NUMBER: US/09/548,372D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
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;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 2043
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-548-372D-7

  Query Match             75.0%;  Score 1552.4;  DB 4;  Length 2043;
  Best Local Similarity   87.6%;  Pred. No. 0;
  Matches 1800;  Conservative    0;  Mismatches  241;  Indels   13;  Gaps    9;

Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
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Db          1 ATGGCCCCAGCGCTGCACTGGCTCCTGCTATGGGTGGGCTCGGGAATGCTGCCTGCCCAG 60

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
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Db         61 GGAACCCATCTCGGCATCCGGCTGCCCCTTCGCAGCGGCCTGGCAGGGCCACCCCTGGGC 120

Qy        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
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Db        121 CTGAGGCTGCCCCGGGAGACTGACGAGGAATCGGAGGAGCCTGGCCGGAGAGGCAGCTTT 180

Qy        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
              |||||||||||||||||||||||||| ||||| || |||||||||| ||||||||||||
Db        181 GTGGAGATGGTGGACAACCTGAGGGGAAAGTCCGGCCAGGGCTACTATGTGGAGATGACC 240

Qy        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
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Db        241 GTAGGCAGCCCCCCACAGACGCTCAACATCCTGGTGGACACGGGCAGTAGTAACTTTGCA 300

Qy        301 GTGGGTGCTGCCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
              ||||| |||||||| ||||| ||||||||||||||||||||||||||||||||||||||
Db        301 GTGGGGGCTGCCCCACACCCTTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
              || || |||||||| |||||||||||||||||||||||||||||||||||| |||||
Db        361 TATCGAGACCTCCGAAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAGGGGGAA 420

Qy        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
              ||||||||||||||| |||||||| ||||||||||||||||||||||||||||||||||
Db        421 CTGGGCACCGACCTGGTGAGCATCCCTCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
              |||||||||||||||| |||||||||||||| || |||||||||| ||||||||
Db        481 GCTGCCATCACTGAATCGGACAAGTTCTTCATCAATGGTTCCAACTGGGAGGGCATCCTA 540

Qy        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
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Db        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCCGACGACTCTTTGGAGCCCTTCTTTGACTCC 600

Qy        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
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Db        601 CTGGTGAAGCAGACCCACATTCCCAACATCTTTTCCCTGCAGCTCTGTGGCGCTGGCTTC 660

Qy        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
              ||||||||||| | || |  |||||||| || ||||||||||||||||||| ||||||
Db        661 CCCCTCAACCAGACCGAGGCACTGGCCTCGGTGGGAGGGAGCATGATCATTGGTGGTATC 720

Qy        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
              |||||||||||  ||||| ||||||||||||||  ||||||||||||||||||||||||||
Db        721 GACCACTCGCTATACACGGGCAGTCTCTGGTACACACCCATCCGGCGGGAGTGGTATTAT 780

Qy        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
              || || |||||||| || ||||| |||||||| || ||||| || ||||||||||||||||

Db        781 GAAGTGATCATTGTACGTGTGGAAATCAATGGTCAAGATCTCAAGATGGACTGCAAGGAG 840

Qy        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
              |||||||| |||||||||||||||||||||||| |||||||||||||  ||||||||||||
Db        841 TACAACTACGACAAGAGCATTGTGGACAGTGGGACCACCAACCTTCGCTTGCCCAAGAAA 900

Qy        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
              || |||||||||||  ||||| ||||||||||||||||||||| ||||||||||||| |||
Db        901 GTATTTGAAGCTGCCGTCAAGTCCATCAAGGCAGCCTCCTCGACGGAGAAGTTCCCGGAT 960

Qy        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
              || ||  |||||||| |||||||||||||||||||||||||||||| ||||||||||||||
Db        961 GGCTTTTGGCTAGGGGAGCAGCTGGTGTGCTGGCAAGCAGGCACGACCCCTTGGAACATT 1020

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Db       1021 TTCCCAGTCATTTCACTTTACCTCATGGGTGAAGTCACCAATCAGTCCTTCCGCATCACC 1080

Qy       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
              ||||||||  |||||||||||  ||||| ||||| ||  |||||||||||||||||||||||||
Db       1081 ATCCTTCCTCAGCAATACCTACGGCCGGTGGAGGACGTGGCCACGTCCCAAGACGACTGT 1140

Qy       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
              ||||||||  ||  |||||||||||||||||||||||||||||||||||  || ||||||||
Db       1141 TACAAGTTCGCTGTCTCACAGTCATCCACGGGCACTGTTATGGGAGCCGTCATCATGGAA 1200

Qy       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
              || ||||| || ||||| ||||| |||||||| |||||||||||||||||||||||||||||
Db       1201 GGTTTCTATGTCGTCTTCGATCGAGCCCGAAAGCGAATTGGCTTTGCTGTCAGCGCTTGC 1260

Qy       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320
              |||||||||||||||||||||||||||||||| || |||||||| || ||||| ||'   ||||||
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Qy       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
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Db       1321 GAAGACTGTGGCTACAACATTCCCCAGACAGATGAGTCAACACTTATGACCATAGCCTAT 1380

Qy       1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440
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Db       1381 GTCATGGCGGCCATCTGCGCCCTCTTCATGTTGCCACTCTGCCTCATGGTATGTCAGTGG 1440

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              |||||||| || |||||||||| ||||| |||||||||||||||||||||||||||||||
Db       1441 CGCTGCCTGCGTTGCCTGCGCCACCAGCACGATGACTTTGCTGATGACATCTCCCTGCTC 1500

Qy       1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
              |||| ||||||| | |||||||| ||| ||||  |||||||||||| ||  |||||||
Db       1501 AAGTAAGGAGGCTCGTGGGCAGATGATGGAGACGCCCCTGGACCACATCTGGGTGGTTCC 1560

Qy       1561 CTTTGGTCACA--AGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCT 1618
              ||||||||||  ||| |||| | ||||| |||||||||||||||||||||||||||||||
Db       1561 CTTTGGTCACATGAGTTGGAGCTATGGATGGTACCTGTGGCCAGAGCACCTCAGGACCCT 1620

Qy       1619 CCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCC 1678
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Db       1621 CACCAACCTGCCAATGCTTCTGGCGTGACAGA-ACAGAGAAATCAGGCAAGCTGGATTAC 1679

Qy       1679 AGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATA 1738
              ||||  || |||||||||| |||| | || |||| ||| |||  |||| |||| ||||||
Db       1680 AGGGCTTGCACCTGTAGGACACAGGAGAGGGAAGGAAGCAGCGTTCTGGTGGCAGGAATA 1739

Qy       1739 CTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAAC 1798
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Db       1740 TCCTTAGGCACCACAAACTTGAGT-TGGAAATTTTGCTGCTTGAAGCTTCAGCCCTGACC 1798

Qy       1799 CTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAG 1858
              || || ||| || |||||||| | |||||||| ||||||||||  | ||     || |||
Db       1799 CTCTGCCCAGCA-TCCTTTAGAGTCTCCAACCTAAAGTATTCTTTATGTC---CTTCCAG 1854

Qy       1859 AAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGA 1918
              |||||||||| ||| || |||| ||||  ||| |||||||||||||||||||||||||||
Db       1855 AAGTACTGGCGTCATACTCAGGCTACC-CGGCATGTGTCCCTGTGGTACCCTGGCAGAGA 1913
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Qy       1919 AGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTA 1978
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Db       1914 AAGGGCCAATC-TCATTCCCTGCTGGCCAAAGTCAGCAGAAGAAGGTG--AAGTTTGCCA 1970

Qy       1979 TTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT 2038
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Db       1971 GTTGCTTTAGTGATAGGGACTGCAGACTCAAGCCT-ACACTGGTACAAAGACTGCGTCTT 2029

Qy       2039 GAATTAAAAAAAAA 2052
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Db       2030 GAGATAAACAAGAA 2043
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RESULT 8
US-09-548-367D-7
; Sequence 7, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
  APPLICANT: GURNEY ET AL.
  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
  TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 2043
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-548-367D-7

Query Match 75.0%; Score 1552.4; DB 4; Length 2043;
Best Local Similarity 87.6%; Pred. No. 0;
Matches 1800; Conservative 0; Mismatches 241; Indels 13; Gaps 9;

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Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
              ||||||| ||| |||| |||||||||||| ||| ||||| ||||| ||||||||||||||
Db          1 ATGGCCCCAGCGCTGCACTGGCTCCTGCTATGGGTGGGCTCGGGAATGCTGCCTGCCCAG 60

            61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
               || ||||| | |||||||||||||||||| |||||||||||||  ||  | ||||||||
Db          61 GGAACCCATCTCGGCATCCGGCTGCCCCTTCGCAGCGGCCTGGCAGGGCCACCCCTGGGC 120

Qy         121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
               ||| ||||||||||||||| ||||| ||  | |||||||| |||||||| ||||||||||
Db         121 CTGAGGCTGCCCCGGGAGACTGACGAGGAATCGGAGGAGCCTGGCCGGAGAGGCAGCTTT 180

Qy         181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
               |||||||||||||||||||||||||| ||||| || |||||||||| ||||||||||||
Db         181 GTGGAGATGGTGGACAACCTGAGGGGAAAGTCCGGCCAGGGCTACTATGTGGAGATGACC 240

Qy         241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
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Db         241 GTAGGCAGCCCCCCCACAGACGCTCAACATCCTGGTGGACACGGGCAGTAGTAACTTTGCA 300

Qy         301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
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Db         301 GTGGGGGCTGCCCCACACCCTTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy         361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
               || || |||||||| |||||||||||||||||||||||||||||||||||| |||||
Db         361 TATCGAGACCTCCGAAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAGGGGGAA 420

Qy         421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
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Db         421 CTGGGCACCGACCTGGTGAGCATCCCTCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy         481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
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Db         481 GCTGCCATCACTGAATCGGACAAGTTCTTCATCAATGGTTCCAACTGGGAGGGCATCCTA 540

Qy         541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
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Qy         601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
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Db         601 CTGGTGAAGCAGACCCACATTCCCAACATCTTTTCCCTGCAGCTCTGTGGCGCTGGCTTC 660

Qy         661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
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Db         661 CCCCTCAACCAGACCGAGGCACTGGCCTCGGTGGGAGGGAGCATGATCATTGGTGGTATC 720

Qy         721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
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Db         721 GACCACTCGCTATACACGGGCAGTCTCTGGTACACACCCATCCGGCGGGAGTGGTATTAT 780

Qy         781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
               || || |||||||| || ||||| |||||||| || ||||| || ||||||||||||||||
Db         781 GAAGTGATCATTGTACGTGTGGAAATCAATGGTCAAGATCTCAAGATGGACTGCAAGGAG 840

Qy         841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
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Db         841 TACAACTACGACAAGAGCATTGTGGACAGTGGGACCACCAACCTTCGCTTGCCCAAGAAA 900

Qy         901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
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Db         901 GTATTTGAAGCTGCCGTCAAGTCCATCAAGGCAGCCTCCTCGACGGAGAAGTTCCCGGAT 960

Qy         961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
               || || |||||||| |||||||||||||||||||||||||||||| ||||||||||||||
Db         961 GGCTTTTGGCTAGGGGAGCAGCTGGTGTGCTGGCAAGCAGGCACGACCCCTTGGAACATT 1020

Qy        1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
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Db        1021 TTCCCAGTCATTTCACTTTACCTCATGGGTGAAGTCACCAATCAGTCCTTCCGCATCACC 1080

Qy        1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
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Db        1081 ATCCTTCCTCAGCAATACCTACGGCCGGTGGAGGACGTGGCCACGTCCCAAGACGACTGT 1140

Qy        1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
               |||||||| ||  |||||||||||||||||||||||||||||||||| || ||||||||
Db        1141 TACAAGTTCGCTGTCTCACAGTCATCCACGGGCACTGTTATGGGAGCCGTCATCATGGAA 1200

Qy        1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
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Db        1201 GGTTTCTATGTCGTCTTCGATCGAGCCCGAAAGCGAATTGGCTTTGCTGTCAGCGCTTGC 1260

Qy        1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320
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Db        1261 CATGTGCACGATGAGTTCAGGACGGCGGCAGTGGAAGGTCCGTTTGTTACGGCAGACATG 1320

Qy        1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
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Db        1321 GAAGACTGTGGCTACAACATTCCCCAGACAGATGAGTCAACACTTATGACCATAGCCTAT 1380

Qy        1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440
               |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1381 GTCATGGCGGCCATCTGCGCCCTCTTCATGTTGCCACTCTGCCTCATGGTATGTCAGTGG 1440

Qy        1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
               |||||||| || |||||||||| ||||| ||||||||||||||||||||||||||||||
Db        1441 CGCTGCCTGCGTTGCCTGCGCCACCAGCACGATGACTTTGCTGATGACATCTCCCTGCTC 1500

Qy        1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
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Db       1501 AAGTAAGGAGGCTCGTGGGCAGATGATGGAGACGCCCCTGGACCACATCTGGGTGGTTCC 1560

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Db       1561 CTTTGGTCACATGAGTTGGAGCTATGGATGGTACCTGTGGCCAGAGCACCTCAGGACCCT 1620

Qy       1619 CCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCC 1678
Db       1621 CACCAACCTGCCAATGCTTCTGGCGTGACAGA-ACAGAGAAATCAGGCAAGCTGGATTAC 1679

Qy       1679 AGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATA 1738
Db       1680 AGGGCTTGCACCTGTAGGACACAGGAGAGGGAAGGAAGCAGCGTTCTGGTGGCAGGAATA 1739

Qy       1739 CTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAAC 1798
Db       1740 TCCTTAGGCACCACAAACTTGAGT-TGGAAATTTTGCTGCTTGAAGCTTCAGCCCTGACC 1798

Qy       1799 CTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAG 1858
Db       1799 CTCTGCCCAGCA-TCCTTTAGAGTCTCCAACCTAAAGTATTCTTTATGTC---CTTCCAG 1854

Qy       1859 AAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGA 1918
Db       1855 AAGTACTGGCGTCATACTCAGGCTACC-CGGCATGTGTCCCTGTGGTACCCTGGCAGAGA 1913

Qy       1919 AGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTA 1978
Db       1914 AAGGGCCAATC-TCATTCCCTGCTGGCCAAAGTCAGCAGAAGAAGGTG--AAGTTTGCCA 1970

Qy       1979 TTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT 2038
Db       1971 GTTGCTTTAGTGATAGGGACTGCAGACTCAAGCCT-ACACTGGTACAAAGACTGCGTCTT 2029

Qy       2039 GAATTAAAAAAAAA 2052
Db       2030 GAGATAAACAAGAA 2043
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RESULT 9
US-09-548-372D-29
; Sequence 29, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 1362
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-548-372D-29

Query Match 65.7%; Score 1359; DB 4; Length 1362;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
Db          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
Db         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120

Qy        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
Db        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
Db        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
Db        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300

Qy        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
Db        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
Db        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
Db        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
Db        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540

Qy        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
Db        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600

Qy        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
Db        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660

Qy        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
Db        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720

Qy        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
Db        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780

Qy        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
Db        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840

Qy        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
Db        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900

Qy        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
Db        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960

Qy        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
Db        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020

Qy       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
Db       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080

Qy       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
Db       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
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Qy       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200

Qy       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260

Qy       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320

Qy       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA 1359
             |||||||||||||||||||||||||||||||||||||||
Db       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA 1359


RESULT 10
US-09-548-367D-29
; Sequence 29, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280H
;  CURRENT APPLICATION NUMBER: US/09/548,367D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
;   LENGTH: 1362
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-548-367D-29

  Query Match           65.7%;  Score 1359;  DB 4;  Length 1362;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1359;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

            1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGGCGCCCCCCTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGGCGCCCCCCTGGGG 120

Qy        121 CTGCGGCTGCCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGCGGCTGCCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300

Qy        301 GTGGGTGCTGCCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGGGTGCTGCCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540

Qy        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600

Qy        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660

Qy        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720

Qy        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780

Qy        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840

Qy        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900

Qy        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960

Qy        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020

Qy       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080

Qy       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140

Qy       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200

Qy       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260

Qy       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320

Qy       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA 1359
              |||||||||||||||||||||||||||||||||||||||
Db       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA 1359


RESULT 11
US-09-548-372D-31
; Sequence 31, Application US/09548372D
; Patent No. 6420534
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; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280I
;  CURRENT APPLICATION NUMBER: US/09/548,372D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
;   LENGTH: 1380
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-548-372D-31

  Query Match             65.7%;  Score 1359;  DB 4;  Length 1380;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1359;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCCTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCCTGGGG 120

Qy        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300

Qy        301 GTGGGTGCTGCCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGGGTGCTGCCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540

Qy        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600

Qy        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660

Qy        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720

Qy        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780

Qy        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840

Qy        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900

Qy        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960

Qy        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020

Qy       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080

Qy       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
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Db       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140

Qy       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200

Qy       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260

Qy       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320

Qy       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA 1359
              |||||||||||||||||||||||||||||||||||||||
Db       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA 1359


RESULT 12
US-09-548-367D-31
; Sequence 31, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280H
;  CURRENT APPLICATION NUMBER: US/09/548,367D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
;   LENGTH: 1380
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-548-367D-31
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  Query Match             65.7%;  Score 1359;  DB 4;  Length 1380;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1359;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGGCGCCCCCCTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGGCGCCCCCCTGGGG 120

Qy        121 CTGCGGCTGCCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGCGGCTGCCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300

Qy        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540

Qy        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600

Qy        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660

              661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720

Qy        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780

Qy        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840

Qy        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900

Qy        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960

Qy        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020

Qy       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080

Qy       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140

Qy       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200

Qy       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260

Qy       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320

Qy       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA 1359
              |||||||||||||||||||||||||||||||||||||||
Db       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA 1359
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RESULT 13
US-09-548-372D-21
; Sequence 21, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280I
;  CURRENT APPLICATION NUMBER: US/09/548,372D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
;   LENGTH: 1341
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-548-372D-21

  Query Match             62.7%;  Score 1297;  DB 4;  Length 1341;
  Best Local Similarity   100.0%;  Pred. No. 9.9e-310;
  Matches 1297;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         63 CACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGGCT 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         42 CACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGGCT 101

Qy        123 GCGGCTGCCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTTGT 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 GCGGCTGCCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTTGT 161

Qy        183 GGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACCGT 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 GGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACCGT 221

Qy        243 GGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCAGT 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 GGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCAGT 281

Qy        303 GGGTGCTGCCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACATA 362
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Db        282 GGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACATA 341

Qy        363 CCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAGCT 422

Db        342 CCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAGCT 401

Qy        423 GGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATTGC 482

Db        402 GGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATTGC 461

Qy        483 TGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTGGG 542

Db        462 TGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTGGG 521

Qy        543 GCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCTCT 602

Db        522 GCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCTCT 581

Qy        603 GGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTCCC 662

Db        582 GGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTCCC 641

Qy        663 CCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATCGA 722

Db        642 CCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATCGA 701

Qy        723 CCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTATGA 782

Db        702 CCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTATGA 761

Qy        783 GGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAGTA 842

Db        762 GGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAGTA 821

Qy        843 CAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAAGT 902

Db        822 CAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAAGT 881

Qy        903 GTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGATGG 962

Db        882 GTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGATGG 941

Qy        963 TTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATTTT 1022

Db        942 TTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATTTT 1001

Qy       1023 CCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACCAT 1082

Db       1002 CCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACCAT 1061

Qy       1083 CCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGTTA 1142

Db       1062 CCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGTTA 1121

Qy       1143 CAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAGGG 1202

Db       1122 CAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAGGG 1181

Qy       1203 CTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGCCA 1262

Db       1182 CTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGCCA 1241

Qy       1263 TGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATGGA 1322

Db       1242 TGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATGGA 1301

Qy       1323 AGACTGTGGCTACAACATTCCACAGACAGATGAGTCA 1359

Db       1302 AGACTGTGGCTACAACATTCCACAGACAGATGAGTCA 1338

RESULT 14
US-09-548-367D-21
; Sequence 21, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280H
;  CURRENT APPLICATION NUMBER: US/09/548,367D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
;   LENGTH: 1341
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-548-367D-21

  Query Match             62.7%;  Score 1297;  DB 4;  Length 1341;
  Best Local Similarity   100.0%;  Pred. No. 9.9e-310;
  Matches 1297;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         63 CACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGGCT 122

Db         42 CACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGGCT 101

Qy        123 GCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTTGT 182

Db        102 GCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTTGT 161

Qy        183 GGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACCGT 242

Db        162 GGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACCGT 221

Qy        243 GGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCAGT 302

Db        222 GGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCAGT 281

Qy        303 GGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACATA 362

Db        282 GGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACATA 341

Qy        363 CCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAGCT 422

Db        342 CCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAGCT 401

Qy        423 GGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATTGC 482

Db        402 GGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATTGC 461

Qy        483 TGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTGGG 542

Db        462 TGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTGGG 521

Qy        543 GCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCTCT 602

Db        522 GCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCTCT 581

Qy        603 GGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTCCC 662

Db        582 GGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTCCC 641

Qy        663 CCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATCGA 722

Db        642 CCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATCGA 701
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Qy        723 CCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTATGA 782
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        702 CCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTATGA 761

Qy        783 GGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAGTA 842
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        762 GGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAGTA 821

Qy        843 CAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAAGT 902
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        822 CAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAAGT 881

Qy        903 GTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGATGG 962
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        882 GTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGATGG 941

Qy        963 TTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATTTT 1022
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        942 TTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATTTT 1001

Qy       1023 CCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACCAT 1082
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1002 CCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACCAT 1061

Qy       1083 CCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGTTA 1142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1062 CCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGTTA 1121

Qy       1143 CAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAGGG 1202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1122 CAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAGGG 1181

Qy       1203 CTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGCCA 1262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1182 CTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGCCA 1241

Qy       1263 TGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATGGA 1322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1242 TGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATGGA 1301

Qy       1323 AGACTGTGGCTACAACATTCCACAGACAGATGAGTCA 1359
              |||||||||||||||||||||||||||||||||||||
Db       1302 AGACTGTGGCTACAACATTCCACAGACAGATGAGTCA 1338
```

RESULT 15
US-09-548-372D-23
; Sequence 23, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 1380
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-548-372D-23

Query Match 62.7%; Score 1297; DB 4; Length 1380;
Best Local Similarity 100.0%; Pred. No. 1e-309;
Matches 1297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         63 CACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGGCT 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 CACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGGCT 140

Qy        123 GCGGCTGCCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTTGT 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 GCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTTGT 200

Qy        183 GGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACCGT 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 GGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACCGT 260

Qy        243 GGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCAGT 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 GGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCAGT 320

Qy        303 GGGTGCTGCCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACATA 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 GGGTGCTGCCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACATA 380

Qy        363 CCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAGCT 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 CCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAGCT 440

Qy        423 GGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATTGC 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATTGC 500

Qy        483 TGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTGGG 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTGGG 560

Qy        543 GCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCTCT 602
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCTCT 620

Qy        603 GGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTCCC 662
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 GGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTCCC 680

Qy        663 CCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATCGA 722
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATCGA 740

Qy        723 CCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTATGA 782
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 CCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTATGA 800

Qy        783 GGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAGTA 842
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAGTA 860

Qy        843 CAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAAGT 902
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 CAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAAGT 920

Qy        903 GTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGATGG 962
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 GTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGATGG 980

Qy        963 TTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATTTT 1022
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arch completed: July  9, 2003, 12:40:28
b time : 104 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 9, 2003, 09:54:12 ; Search time 5392 Seconds
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Title: US-09-869-414A-3
Perfect score: 2070
Sequence: 1 atggcccaagccctgccctg.....aaaaaaaaaaaaaaaaaaaa 2070

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2070	100.0	2070	6	AX378015	AX378015 Sequence
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4	2062	99.6	2526	9	AF190725	AF190725 Homo sapi
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7	2032	98.2	2541	6	AR178469	AR178469 Sequence
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15	1887.2	91.2	1977	6	AX105387	AX105387 Sequence
16	1887.2	91.2	1977	6	AX378017	AX378017 Sequence
17	1843.4	89.1	2370	6	AR178470	AR178470 Sequence
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ALIGNMENTS

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LOCUS AX105385 2070 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 3 from Patent WO0123533.
ACCESSION AX105385
VERSION AX105385.1 GI:13921511
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2070)
AUTHORS Gurney,M. and Bienkowski,M.J.
TITLE Alzheimer's disease secretase, app substrates therefor, and uses therefor

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  JOURNAL   Patent: WO 0123533-A 3 05-APR-2001;
            Pharmacia & Upjohn Company (US)
FEATURES             Location/Qualifiers
     source          1. .2070
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BASE COUNT      476 a    583 c    562 g    449 t
ORIGIN

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RESULT 2
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DEFINITION  Sequence 1 from Patent WO0206306.
ACCESSION   AX378015
VERSION     AX378015.1  GI:19574050
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE 1
  AUTHORS   Yan,R., Tomasselli,A.G., Gurney,M.E., Emmons,T.L., Bienkowski,M.J.
            and Heinrikson,R.L.
  TITLE     Substrates and assays for _g(b)-secretase activity
  JOURNAL   Patent: WO 0206306-A 1 24-JAN-2002;
            PHARMACIA & UPJOHN COMPANY (US)
FEATURES             Location/Qualifiers
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BASE COUNT      476 a    583 c    562 g    449 t
ORIGIN

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  Matches 2070;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
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Db        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720

Qy        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
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Qy        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
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Qy        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
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Qy       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
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Qy       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
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Db       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140

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Qy       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
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Qy       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
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Qy       1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
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Db       1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800

Qy       1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
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RESULT 3
AF200343
LOCUS       AF200343               2070 bp    mRNA    linear   PRI 12-DEC-1999
DEFINITION  Homo sapiens chromosome 11 aspartyl protease 2 mRNA, complete cds.
ACCESSION   AF200343
VERSION     AF200343.1  GI:6561813
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2070)
  AUTHORS   Yan,R., Bienkowski,M.J., Shuck,M.E., Miao,H., Tory,M.C.,
            Pauley,A.M., Brashier,J.R., Stratman,N.C., Mathews,W.R., Buhl,A.E.,
            Carter,D.B., Tomasselli,A.G., Parodi,L.A., Heinrikson,R.L. and
            Gurney,M.E.
  TITLE     Membrane-anchored aspartyl protease with Alzheimer's disease
            beta-secretase activity
  JOURNAL   Nature 402 (6761), 533-537 (1999)
  MEDLINE   20057170
   PUBMED   10591213
REFERENCE   2  (bases 1 to 2070)
  AUTHORS   Bienkowski,M.J., Shuck,M.E., Slightom,J.L. and Drong,R.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-OCT-1999) Genomics Research, Pharmacia&Upjohn, 301
            Henrietta, Kalamazoo, MI 49007, USA
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                     /chromosome="11"
                     /map="11q23.3-24.1"
     CDS             1. .1506
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                     /db_xref="GI:6561814"
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                     AAPHPFLHRYYQRQLSSTYRDLRKGVYVPYTQGKWEGELGTDLVSIPHGPNVTVRANI
                     AAITESDKFFINGSNWEGILGLAYAEIARPDDSLEPFFDSLVKQTHVPNLFSLQLCGA
                     GFPLNQSEVLASVGGSMIIGGIDHSLYTGSLWYTPIRREWYYEVIIVRVEINGQDLKM
                     DCKEYNYDKSIVDSGTTNLRLPKKVFEAAVKSIKAASSTEKFPDGFWLGEQLVCWQAG
                     TTPWNIFPVISLYLMGEVTNQSFRITILPQQYLRPVEDVATSQDDCYKFAISQSSTGT
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BASE COUNT      476 a    582 c    563 g    449 t
ORIGIN
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  Query Match           99.9%;  Score 2068.4;  DB 9;  Length 2070;
  Best Local Similarity 100.0%;  Pred. No. 0;
  Matches 2069;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120

Qy        121 CTGCGGCTGCCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGCGGCTGCCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy        241 GTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
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Db        241 GTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300

Qy        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
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Db        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
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Db        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
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Db        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
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Db        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540

Qy        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
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Db        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600

Qy        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGCTTC 660

Qy        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720

Qy        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780

Qy        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
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Db        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840

Qy        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
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Db        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900

Qy        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
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Db        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960

Qy        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
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Db        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020

Qy       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
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Db       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080

Qy       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
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Db       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140

Qy       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
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Db       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200

Qy       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
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Qy       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320
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Db       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320

Qy       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
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Qy       1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680
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Qy       1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
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Qy       1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
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Qy       2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
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Db       2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070


RESULT 4
AF190725
LOCUS       AF190725                2526 bp    mRNA    linear   PRI 26-OCT-1999
DEFINITION  Homo sapiens beta-site APP cleaving enzyme (BACE) mRNA, complete
            cds.
ACCESSION   AF190725
VERSION     AF190725.1  GI:6118538
KEYWORDS    .
SOURCE      Homo sapiens.
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2526)
  AUTHORS   Vassar,R., Bennett,B.D., Babu-Khan,S., Kahn,S., Mendiaz,E.A.,
            Denis,P., Teplow,D.B., Ross,S., Amarante,P., Loeloff,R., Luo,Y.,
            Fisher,S., Fuller,J., Edenson,S., Lile,J., Jarosinski,M.A.,
            Biere,A.L., Curran,E., Burgess,T., Louis,J.C., Collins,F.,
            Treanor,J., Rogers,G. and Citron,M.
  TITLE     Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
            the transmembrane aspartic protease BACE
  JOURNAL   Science 286 (5440), 735-741 (1999)
  MEDLINE   20002972
   PUBMED   10531052
REFERENCE   2  (bases 1 to 2526)
  AUTHORS   Bennett,B.D., Vassar,R. and Citron,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-SEP-1999) Neuroscience, Amgen Inc., One Amgen Center
            Dr., Thousand Oaks, CA 91320-1799, USA
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BASE COUNT      534 a    781 c    715 g    496 t
ORIGIN

  Query Match             99.6%;  Score 2062;  DB 9;  Length 2526;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 2065;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 513

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 573

Qy        121 CTGCGGCTGCCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
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Db      814 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 873

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Db      1114 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 1173

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Qy      1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
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Db      2194 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 2253

Qy      1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
Db      2254 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 2313

Qy      1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
Db      2314 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 2373

Qy      1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
Db      2374 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 2433

Qy      1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
Db      2434 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2493

Qy      2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
Db      2494 ATTAAAAAAAAAAACTAGAAAAAAAAAAAA 2523
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RESULT 5
AF201468

LOCUS	AF201468 5878 bp mRNA linear PRI 19-DEC-1999
DEFINITION	Homo sapiens APP beta-secretase mRNA, complete cds.
ACCESSION	AF201468
VERSION	AF201468.1 GI:6601444
KEYWORDS	.
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 5878)
AUTHORS	Sinha,S., Anderson,J.P., Barbour,R., Basi,G.S., Caccavello,R., Davis,D., Doan,M., Dovey,H.F., Frigon,N., Hong,J., Jacobson-Croak,K., Jewett,N., Keim,P., Knops,J., Lieberburg,I., Power,M., Tan,H., Tatsuno,G., Tung,J., Schenk,D., Seubert,P.,

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            Suomensaari,S., Wang,S., Walker,D., Zhao,J., McConlogue,L. and
            John,V.
  TITLE     Purification and cloning of amyloid precursor protein
            beta-secretase from human brain
  JOURNAL   Nature 402 (6761), 537-540 (1999)
  MEDLINE   20057171
   PUBMED   10591214
REFERENCE   2  (bases 1 to 5878)
  AUTHORS   Basi,G.S., Power,M.D., Wang,S., Tatsuno,G., Frigon,N., Doan,M.,
            Hong,G., Keim,P., Anderson,J., Sinha,S. and McConlogue,L.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-NOV-1999) Gene Expression Group, Elan
            Pharmaceuticals, Inc., 800 Gateway Blvd., S. San Francisco, CA
            94080, USA
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                     /note="membrane type aspartyl protease"
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                     AAITESDKFFINGSNWEGILGLAYAEIARPDDSLEPFFDSLVKQTHVPNLFSLQLCGA
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BASE COUNT     1547 a   1518 c   1405 g   1408 t
ORIGIN

  Query Match           99.2%;  Score 2052.6;  DB 9;  Length 5878;
  Best Local Similarity 99.8%;  Pred. No. 0;
  Matches 2055;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
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Db        455 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 514

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
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Qy        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
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Db        935 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 994

Qy        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
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Qy        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
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Db       1055 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGCTTC 1114

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Qy        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
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Db       1235 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 1294

Qy        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
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Db       1535 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1594

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RESULT 6
AB032975
LOCUS       AB032975               5814 bp    mRNA    linear   PRI 17-MAY-2001
DEFINITION  Homo sapiens mRNA for KIAA1149 protein, partial cds.
ACCESSION   AB032975
VERSION     AB032975.2  GI:14133242
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REFERENCE   1  (sites)
  AUTHORS   Hirosawa,M., Nagase,T., Ishikawa,K., Kikuno,R., Nomura,N. and
            Ohara,O.
  TITLE     Characterization of cDNA clones selected by the GeneMark analysis
            from size-fractionated cDNA libraries from human brain
  JOURNAL   DNA Res. 6 (5), 329-336 (1999)
  MEDLINE   20039618
REFERENCE   2  (bases 1 to 5814)
  AUTHORS   Ohara,O., Nagase,T. and Kikuno,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-OCT-1999) Osamu Ohara, Kazusa DNA Research Institute,
            Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba
            292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
            URL:http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913,
            Fax:+81-438-52-3914)
COMMENT     On May 17, 2001 this sequence version replaced gi:6330044.
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                     TGSLWYTPIRREWYYEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRLPKKVFE
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ORIGIN
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Query Match 98.6%; Score 2040; DB 9; Length 5814;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2054; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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Db       443 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 502

Qy        61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCT-GGGGGGCGCCCCCCTGGG 119
             |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db       503 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGGCGCCCCCCTGGG 562

Qy       120 GCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTT 179
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       563 GCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTT 622

Qy       180 TGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGAC 239
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       623 TGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGAC 682

Qy       240 CGTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGC 299
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Qy       300 AGTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCAC 359
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Qy       360 ATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGA 419
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       803 ATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGA 862

Qy       420 GCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACAT 479
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       863 GCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACAT 922

Qy       480 TGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCT 539
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       923 TGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCT 982

Qy       540 GGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTC 599
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       983 GGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTC 1042

Qy       600 TCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTT 659
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Db      1043 TCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGCTT 1102

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Db      1103 CCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTAT 1162

Qy       720 CGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTA 779
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Qy       780 TGAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGA 839
Db      1223 TGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGA 1282

Qy       840 GTACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAA 899
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Qy       960 TGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACAT 1019
Db      1403 TGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACAT 1462

Qy      1020 TTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCAC 1079
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Qy      1260 CCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACAT 1319
Db      1703 CCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACAT 1762

Qy      1320 GGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTA 1379
Db      1763 GGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTA 1822

Qy      1380 TGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTG 1439
Db      1823 TGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTG 1882

Qy      1440 GCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCT 1499
Db      1883 GCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCT 1942

Qy      1500 GAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTC 1559
Db      1943 GAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTC 2002

Qy      1560 ACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTC 1619
Db      2003 ACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTC 2062

Qy      1620 CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCA 1679
Db      2063 CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCA 2122

Qy      1680 GGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATAC 1739
Db      2123 GGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATAC 2182

Qy      1740 TCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACC 1799
Db      2183 TCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACC 2242

Qy      1800 TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGA 1859
Db      2243 TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGA 2302

Qy      1860 AGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAA 1919
Db      2303 AGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAA 2362

Qy      1920 GAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTAT 1979
Db      2363 GAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTAT 2422

Qy      1980 TTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTG 2039
Db      2423 TTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTG 2482

Qy      2040 AATTAAAAAAAAAAAAAAAA 2059
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DEFINITION  Sequence 1 from patent US 6319689.
ACCESSION   AR178469
VERSION     AR178469.1  GI:20219607
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2541)
  AUTHORS   Powell,D.J., Chapman,C.G., Murphy,K. and Smith,T.S.
  TITLE     ASP2
  JOURNAL   Patent: US 6319689-A 1 20-NOV-2001;
FEATURES             Location/Qualifiers
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BASE COUNT      598 a    673 c    675 g    579 t     16 others
ORIGIN

  Query Match           98.2%;  Score 2032;  DB 6;  Length 2541;
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  Matches 2049;  Conservative    0;  Mismatches   10;  Indels    1;  Gaps    1;

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Db          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
Db         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120

Qy        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
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Qy        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
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Qy        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
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Qy        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
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Db        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
Qy        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
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Qy        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
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Qy        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
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Qy        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
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Qy       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
Db       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
Qy       1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440
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Qy       1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
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Qy       1800 TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGA 1859
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Qy       1980 TTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTG 2039
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Qy       2040 AATTAAAAAAAAAAAAAAAA 2059
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DEFINITION  Sequence 1 from Patent EP0855444.
ACCESSION   AX002655
VERSION     AX002655.1  GI:7242133
KEYWORDS    .
SOURCE      unidentified.
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            unclassified.
REFERENCE   1  (bases 1 to 2541)
  AUTHORS   Murphy,K. and Chapman,C.G.
  TITLE     Aspartic proteinase 2 (ASP2)
  JOURNAL   Patent: EP 0855444-A 1 29-JUL-1998;
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BASE COUNT      598 a    673 c    675 g    579 t     16 others
ORIGIN

  Query Match           98.2%;  Score 2032;  DB 6;  Length 2541;
  Best Local Similarity  99.5%;  Pred. No. 0;
  Matches 2049;  Conservative    0;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
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Db          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120

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Qy       1740 TCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACC 1799

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Qy       2040 AATTAAAAAAAAAAAAAAAA 2059

Db       2041 AATTAAAAAAAAAAACTAGA 2060
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RESULT 9
E50816
LOCUS E50816 2541 bp DNA linear PAT 18-JUN-2001
DEFINITION Aspartate proteinase ASP2.
ACCESSION E50816
VERSION E50816.1 GI:13023199

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KEYWORDS    JP 2000060579-A/1.
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2541)
  AUTHORS   David,J.P., Conrad,G.C., Kay,M. and Trudy,S.S.
  TITLE     Aspartate proteinase ASP2
  JOURNAL   Patent: JP 2000060579-A 1 29-FEB-2000;
            SMITHKLINE BEECHAM CORP
COMMENT     OS   Unidentified
            PN   JP 2000060579-A/1
            PD   29-FEB-2000
            PF   03-AUG-1999 JP 1999219665
            PR   28-JAN-1997 GB    9701684:4
            PI   DAVID J POWERU,CONRAD G CHAPPUMAN,KAY MAFI,TRUDY S SMITH PC
            C12N15/09,A61K31/7088,A61K38/46,A61K39/00,A61K39/395, PC
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BASE COUNT      598 a    673 c    675 g    579 t     16 others
ORIGIN

  Query Match           98.2%;  Score 2032;  DB 6;  Length 2541;
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  Matches 2049;  Conservative    0;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCCTGGGG 120
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Db        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300

Qy        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
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Qy        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
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Qy        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
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Qy        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
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Qy       1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440
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Db       2041 AATTAAAAAAAAAAACTAGA 2060
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RESULT 10
AX062111
LOCUS AX062111 3252 bp DNA linear PAT 24-JAN-2001
DEFINITION Sequence 1 from Patent WO0100665.
ACCESSION AX062111
VERSION AX062111.1 GI:12540032
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3252)
AUTHORS Tang,J.J., Hong,L. and Ghosh,A.K.
TITLE Inhibitors of memapsin 2 and use thereof
JOURNAL Patent: WO 0100665-A 1 04-JAN-2001;
Oklahoma Medical Research Foundation (US) ; THE BOARD OF TRUSTEES
OF THE UNIVERSITY OF ILLINOIS (US)
FEATURES Location/Qualifiers
source 1. .3252
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/db_xref="taxon:9606"
BASE COUNT 804 a 863 c 811 g 771 t 3 others
ORIGIN

Query Match 97.1%; Score 2010; DB 6; Length 3252;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2013; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy        220 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGAT 279
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Qy        640 CACCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGG 699
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Qy        700 AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC 759
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Qy       1060 AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG 1119
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Qy       1120 GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT 1179
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RESULT 11
AX063201
LOCUS       AX063201               3252 bp    DNA     linear   PAT 24-JAN-2001
DEFINITION  Sequence 1 from Patent WO0100663.
ACCESSION   AX063201
VERSION     AX063201.1  GI:12541045
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3252)
  AUTHORS   Tang,J.J., Lin,X. and Koelsch,G.
  TITLE     Catalytically active recombinant memapsin and methods of use there
            of
  JOURNAL   Patent: WO 0100663-A 1 04-JAN-2001;
            Oklahoma Medical Research Foundation (US)
FEATURES             Location/Qualifiers
     source          1. .3252
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BASE COUNT      804 a    863 c    811 g    771 t      3 others
ORIGIN

  Query Match           97.1%;  Score 2010;  DB 6;  Length 3252;
  Best Local Similarity 99.8%;  Pred. No. 0;
  Matches 2013;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

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Qy        100 CTGGGGGGCGCCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAG 159
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Qy        160 CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 219
Db        121 CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 180

Qy        220 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 279
Db        181 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 240

Qy        280 ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTAC 339
Db        241 ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTAC 300

Qy        340 CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC 399
Db        301 CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC 360

Qy        400 CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC 459
Db        361 CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC 420

Qy        460 GTCACTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC 519
Db        421 GTCACTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC 480

Qy        520 TCCAACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC 579
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Qy        640 CACCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGG 699
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Qy        700 AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC 759
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Qy        760 ATCCGGCGGGAGTGGTATTATGAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGAT 819
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Qy        880 AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC 939
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Qy        940 TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA 999
Db        901 TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA 960

Qy       1000 GGCACCACCCCTTGGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC 1059
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Db        961 GGCACCACCCCTTGGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC 1020

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Qy       1360 ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC 1419
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Qy       1420 TGCCTCATGGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT 1479
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Qy       1480 GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT 1539
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Qy       1660 GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG 1719
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Db       1621 GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG 1680

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RESULT 12
AX472368

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LOCUS       AX472368               3252 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 1 from Patent WO02053594.
ACCESSION   AX472368
VERSION     AX472368.1  GI:22207364
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ghosh,A.K., Koelsch,G. and Tang,J.J.
  TITLE     Inhibitors of memapsin 2 and use thereof
  JOURNAL   Patent: WO 02053594-A 1 11-JUL-2002;
            OKLAHOMA MED RES FOUND (US); TRUSTEES OF THE UNIVERSITY OF ILLINOIS
            (US)
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
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BASE COUNT      804 a    863 c    811 g    771 t      3 others
ORIGIN

  Query Match             97.1%;  Score 2010;  DB 6;  Length 3252;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 2013;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

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Qy       880 AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC 939
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Qy      1600 CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA 1659
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Qy      1960 GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT 2019
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Qy      2020 GGTGCAAAGATTGCCTCTTGAATTAAAAAAAAAAAAAA 2057
Db       1981 GGTGCAAAGATTGCCTCTTGAATTAAAAAAAAACTAGA 2018
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RESULT 13
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LOCUS       AF200193               3252 bp    mRNA    linear   PRI 16-FEB-2000
DEFINITION  Homo sapiens memapsin 2 mRNA, partial cds.
ACCESSION   AF200193
VERSION     AF200193.1  GI:6470292
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3252)
  AUTHORS   Lin,X., Koelsch,G., Wu,S., Downs,D., Dashti,A. and Tang,J.
  TITLE     Human aspartic protease memapsin 2 cleaves the beta-secretase site
            of beta-amyloid precursor protein
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1456-1460 (2000)
  MEDLINE   20144060
   PUBMED   10677483
REFERENCE   2  (bases 1 to 3252)
  AUTHORS   Lin,X., Koelsch,G. and Tang,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-OCT-1999) Protein Studies Program, Oklahoma Medical
            Research Foundation, 825 N.E. 13th Street, Oklahoma City, OK 73104,
            USA
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  Query Match          97.1%;  Score 2010;  DB 9;  Length 3252;
  Best Local Similarity   99.8%;  Pred. No. 0;
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Qy        160 CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 219
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Qy        220 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 279
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Qy        280 ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTAC 339
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Db        241 ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTAC 300

Qy        340 CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC 399
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          361 CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC 420

Qy        460 GTCACTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC 519
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Qy        520 TCCAACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC 579
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Qy        580 CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG 639
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Db        541 CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG 600

Qy        640 CACCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGG 699
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Db        601 CAGCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGG 660

Qy        700 AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC 759
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Db        661 AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC 720

Qy        760 ATCCGGCGGGAGTGGTATTATGAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGAT 819
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          781 CTGAAAATGGACTGCAAGGAGTACAACTATGACAAGAGCATTGTGGACAGTGGCACCACC 840

Qy        880 AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC 939
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Qy        940 TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA 999
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Qy       1000 GGCACCACCCCTTGGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC 1059
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Qy       1060 AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG 1119
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Qy       1180 ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT 1239
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Qy       1540 GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC 1599
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Db       1501 GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC 1560

Qy       1600 CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA 1659
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Db       1861 TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA 1920

Qy       1960 GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT 2019
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Db       1921 GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT 1980

Qy       2020 GGTGCAAAGATTGCCTCTTGAATTAAAAAAAAAAAAAA 2057
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Db       1981 GGTGCAAAGATTGCCTCTTGAATTAAAAAAAAACTAGA 2018
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RESULT 14
AX364933
LOCUS       AX364933               5757 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 84 from Patent WO0206315.
ACCESSION   AX364933
VERSION     AX364933.1  GI:18696823
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Mintz,L., Freilich,S. and Bernstein,J.
```

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  TITLE     Novel nucleic acid and amino acid sequences
  JOURNAL   Patent: WO 0206315-A 84 24-JAN-2002;
            Compugen Ltd. (IL)
FEATURES             Location/Qualifiers
     source          1. .5757
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     1485 a   1490 c   1392 g   1388 t      2 others
ORIGIN

  Query Match             91.5%;  Score 1894.2;  DB 6;  Length 5757;
  Best Local Similarity   96.2%;  Pred. No. 0;
  Matches 1981;  Conservative    0;  Mismatches    3;  Indels   75;  Gaps    1;

Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        455 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 514

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
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Qy        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
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Qy        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
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Qy        241 GTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
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Qy        301 GTGGGTGCTGCCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
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Db        755 GTGGGTGCTGCCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 814

Qy        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
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Db        815 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 874

Qy        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
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Db        875 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 934

Qy        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
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Qy        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
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Db       1022 ----------------------------------------CTTTGTGGTGCTGGCTTC 1039

Qy        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
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Db       1040 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 1099

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Qy        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
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Qy       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
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Qy       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
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Db       1460 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1519

Qy       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
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Qy       1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440
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Db       2120 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 2179

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Db       2360 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2419

Qy       2041 ATTAAAAAAAAAAAAAAAA 2059
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RESULT 15
AX105387
LOCUS       AX105387               1977 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 5 from Patent WO0123533.
ACCESSION   AX105387
VERSION     AX105387.1  GI:13921512
KEYWORDS    .
SOURCE      human.
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE 1  (bases 1 to 1977)
  AUTHORS   Gurney,M. and Bienkowski,M.J.
  TITLE     Alzheimer's disease secretase, app substrates therefor, and uses
            therefor
  JOURNAL   Patent: WO 0123533-A 5 05-APR-2001;
            Pharmacia & Upjohn Company (US)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606" .
BASE COUNT      447 a    552 c    551 g    427 t
ORIGIN

  Query Match             91.2%;  Score 1887.2;  DB 6;  Length 1977;
  Best Local Similarity   96.2%;  Pred. No. 0;
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Db        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

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Db        541 GGGCTGGCCTATGCTGAGATTGCCAGG------------------------------- 567

Qy        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
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Qy        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
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Qy        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
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Qy        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
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Qy        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
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Qy        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
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Qy       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
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Qy       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320
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Qy       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
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Qy       1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680
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Qy       2041 ATTAAAAAAAAA 2052
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Db       1966 AAAAAAAAAAAA 1977
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Search completed: July 9, 2003, 14:10:34
Job time : 5398 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 8, 2003, 18:07:46 ; Search time 467 Seconds
(without alignments)
9982.091 Million cell updates/sec

Title: US-09-869-414A-3
Perfect score: 2070
Sequence: 1 atggcccaagccctgccctg.....aaaaaaaaaaaaaaaaaaa 2070

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2070	100.0	2070	21	AAA15662	Human aspartyl pro
2	2070	100.0	2070	22	AAD17865	Human aspartyl pro
3	2070	100.0	2070	22	AAD13021	Human aspartyl pro
4	2070	100.0	2070	22	AAS11517	Human cDNA encodin
5	2070	100.0	2070	22	AAS11702	DNA encoding human
6	2070	100.0	2070	22	AAD06739	Human aspartyl pro
7	2070	100.0	2070	24	ABL52457	Human Asp-2(a) nuc
8	2070	100.0	2070	24	ABL49914	Human aspartyl pro
9	2047.8	98.9	16080	21	AAA59553	DNA clone pCEK C1.
10	2039.8	98.5	2348	21	AAA59551	DNA encoding a hum
11	2032	98.2	2541	19	AAV41696	Nucleotide sequenc
12	2010	97.1	3252	22	AAF31848	Human memapsin 2 c
13	2010	97.1	3252	22	AAF28101	Memapsin 2 DNA. H
14	2010	97.1	3252	24	ABK88641	cDNA encoding huma
15	1894.2	91.5	5757	24	ABL39774	Human NS cDNA sequ
16	1887.2	91.2	1977	21	AAA15663	Human aspartyl pro
17	1887.2	91.2	1977	22	AAD17866	Human aspartyl pro
18	1887.2	91.2	1977	22	AAD13022	Human aspartyl pro
19	1887.2	91.2	1977	22	AAS11518	Human cDNA encodin
20	1887.2	91.2	1977	22	AAS11703	DNA encoding human
21	1887.2	91.2	1977	22	AAD06740	Human aspartyl pro
22	1887.2	91.2	1977	24	ABL52458	Human Asp-2(b) nuc
23	1887.2	91.2	1977	24	ABL49915	Human aspartyl pro
24	1843.4	89.1	2370	19	AAV41697	Partial nucleotide
25	1788.8	86.4	1979	22	AAK94824	Human full-length
26	1644.8	79.5	1747	20	AAX97602	Extended human sec
27	1552.4	75.0	2043	21	AAA15664	Murine aspartyl pr
28	1552.4	75.0	2043	22	AAD17867	Murine aspartyl pr
29	1552.4	75.0	2043	22	AAD13023	Murine aspartyl pr
30	1552.4	75.0	2043	22	AAS11519	Mouse cDNA encodin
31	1552.4	75.0	2043	22	AAS11704	DNA encoding mouse
32	1552.4	75.0	2043	22	AAD06741	Murine aspartyl pr
33	1552.4	75.0	2043	24	ABL52459	Mouse Asp-2(a) nuc
c 34	1501.2	72.5	2907	23	AAS82237	DNA encoding novel
35	1499.8	72.5	1503	21	AAA28278	Human cDNA encodin
36	1499.8	72.5	1503	21	AAA59550	DNA encoding a hum
37	1499.8	72.5	1527	24	ABA02406	FLAG-tagged human
38	1487.4	71.9	1911	22	AAD09485	Human aspartyl pro
39	1423	68.7	2914	23	AAS73798	DNA encoding novel
40	1395.4	67.4	2158	24	ABK63758	Rat sequence diffe
41	1359	65.7	1362	21	AAA15688	Modified human asp
42	1359	65.7	1362	22	AAD17878	Human-Asp 2(a) pro
43	1359	65.7	1362	22	AAD13034	Human-Asp2(a) delt
44	1359	65.7	1362	22	AAS11530	Human cDNA encodin
45	1359	65.7	1362	22	AAS11715	DNA encoding human

ALIGNMENTS

RESULT 1
AAA15662
ID AAA15662 standard; cDNA; 2070 BP.
XX
AC AAA15662;
XX
DT 03-AUG-2000 (first entry)
XX
DE Human aspartyl protease 2 (a) (Asp2) nucleotide sequence.
XX
KW Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;
KW Alzheimer's disease; beta secretase site; ss.
XX
OS Homo sapiens.
XX
PN WO200017369-A2.
XX
PD 30-MAR-2000.
XX
PF 23-SEP-1999; 99WO-US20881.
XX
PR 24-SEP-1998; 98US-0101594.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Gurney ME, Bienkowski MJ, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2000-303209/26.
DR P-PSDB; AAY88425.
XX
PT New enzyme designated human aspartase useful in research into
PT Alzheimer's Disease is capable of cleaving amyloid protein precursor at

PT the beta secretase site to produce amyloid beta peptide -
XX
PS Claim 5; Fig 2; 183pp; English.
XX
CC This sequence represents the human aspartyl protease 2 (Asp2) nucleotide
CC sequence. The invention relates to a protease (e.g. Asp2) capable of
CC cleaving the beta secretase site of amyloid precursor protein (APP). The
CC protease contains a sequence encoding the amino acid sequence DTG and a
CC sequence encoding DSG or DTG separated by 100-300 amino acids. When
CC mutated the APP gene causes an autosomal dominant form of Alzheimer's
CC disease. APP localises to the cell surface membrane and have a single
CC C-terminal transmembrane domain. Proteolytic processing of APP produces
CC the amyloid beta protein, which is possibly very important in Alzheimer's
CC disease. The invention includes a nucleotide sequence encoding the
CC protease, a vector containing the nucleotide sequence, and a cell line
CC comprising the vector. Methods for screening for inhibitors of beta
CC secretase activity are also given in the invention. The human aspartase
CC protein and nucleotide sequences and the methods for identifying
CC inhibitors of the protease, are useful in the treatment of and research
CC in to Alzheimer's disease.
XX
SQ Sequence 2070 BP; 476 A; 583 C; 562 G; 449 T; 0 other;

Query Match 100.0%; Score 2070; DB 21; Length 2070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
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Qy        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
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Qy        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
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Qy        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
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Qy        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
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Qy        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
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Qy        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
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Qy        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
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Db       1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680

Qy       1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740

Qy       1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
```

```
Qy       1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860

Qy       1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920

Qy       1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980

Qy       1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040

Qy       2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
             ||||||||||||||||||||||||||||||
Db       2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
```

RESULT 2
AAD17865
ID AAD17865 standard; cDNA; 2070 BP.
XX
AC AAD17865;
XX
DT 10-DEC-2001 (first entry)
XX
DE Human aspartyl protease 2(a) [hu-Asp2(a)] cDNA.
XX
KW Human; aspartyl protease 2(a); Asp2(a); amyloid precursor protein; APP;
KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;
KW chromosome 11q23.3-24.1; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1..1506
FT   /*tag= a
FT   /product= "Human aspartyl protease 2(a)"
FT sig_peptide   1..63
FT   /*tag= b
FT mat_peptide   64..1503
FT   /*tag= c
FT   /product= "Mature human aspartyl protease 2(a)"
XX
PN GB2357767-A.
XX
PD 04-JUL-2001.
XX
PF 22-SEP-2000; 2000GB-0023315.
XX
PR 23-SEP-1999; 99US-0155493.
PR 23-SEP-1999; 99US-0404133.
PR 23-SEP-1999; 99WO-US20881.
PR 13-OCT-1999; 99US-0416901.
PR 06-DEC-1999; 99US-0169232.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Bienkowkski MJ, Gurney M;
XX
DR WPI; 2001-444208/48.
DR P-PSDB; AAE10629.
XX
PT Polypeptide comprising fragments of human aspartyl protease with
PT amyloid precursor protein processing activity and alpha-secretase
PT activity, for identifying modulators useful in treating Alzheimer's
PT disease -
XX
PS Example 2; Fig 2; 187pp; English.
XX
CC The patent discloses human aspartyl protease 1 (hu-Asp1) or modified
CC Asp1 proteins which lack transmembrane domain or amino terminal
CC domain or cytoplasmic domain and retains alpha-secretase activity
CC and amyloid protein precursor (APP) processing activity. The proteins
CC of the invention are useful for assaying hu-Asp1 alpha-secretase
CC activity, which in turn is useful for identifying modulators of
CC hu-Asp1 alpha-secretase activity, where modulators that increase
CC hu-Asp1 alpha-secretase activity are useful for treating Alzheimer's
CC disease (AD) which causes progressive dementia with consequent
CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
CC neuronal loss. Hu-Asp1 protease substrate is useful for assaying
CC hu-Asp1 proteolytic acti0ity, by contacting hu-Asp1 protein with
CC the substrate under acidic conditions and determining the level of
CC hu-Asp1 proteolytic activity. The present sequence is a cDNA encoding
CC long form of human Asp2 protein, designated as Asp2(a). Asp2 gene is
CC localised on chromosome 11q23.3-24.1.
XX
SQ Sequence 2070 BP; 476 A; 583 C; 562 G; 449 T; 0 other;

```
  Query Match             100.0%;  Score 2070;  DB 22;  Length 2070;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2070;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120

Qy        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300

Qy        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540

Qy        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600

Qy        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660

Qy        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
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Qy       721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
Db       721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780

Qy       781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
Db       781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840

Qy       841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
Db       841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900

Qy       901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
Db       901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960

Qy       961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
Db       961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020

Qy      1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
Db      1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080

Qy      1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
Db      1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140

Qy      1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
Db      1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200

Qy      1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
Db      1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260

Qy      1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320
Db      1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320

Qy      1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
Db      1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380

Qy      1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440
Db      1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440

Qy      1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
Db      1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500

Qy      1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
Db      1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560

Qy      1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620
Db      1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620

Qy      1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680
Db      1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680

Qy      1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740
Db      1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740

Qy      1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
Db      1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800

Qy      1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
Db      1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860

Qy      1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
Db      1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920

Qy      1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
Db      1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980

Qy      1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
Db      1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040

Qy      2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
Db      2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
```

RESULT 3
AAD13021
ID AAD13021 standard; cDNA; 2070 BP.
XX
AC AAD13021;
XX
DT 23-OCT-2001 (first entry)
XX
DE Human aspartyl protease 2a (Hu-Asp2a) cDNA.
XX
KW Human; aspartyl protease 2a; Asp 2a; beta-amyloid precursor protein; APP;
KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;
KW neuroprotective; antisense therapy; gene therapy;
KW chromosome 11q23.3-24.1; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1..1506
FT   /*tag= a
FT   /product= "Human aspartyl protease 2a (Hu-Asp2a)"
FT sig_peptide   1..63
FT   /*tag= b
FT mat_peptide   64..1503
FT   /*tag= c
FT   /product= "Mature human aspartyl protease 2a (Hu-Asp2a)"
XX
PN WO200150829-A2.
XX
PD 19-JUL-2001.
XX
PF 09-MAY-2001; 2001WO-IB00799.
XX
PR 09-MAY-2001; 2001WO-IB00799.
XX
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2001-483072/52.
DR P-PSDB; AAE06859.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity -
XX
PS Claim 98; Fig 2; 185pp; English.

XX
CC The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC precursor protein (APP) isoforms and their corresponding DNA molecules.
CC Human aspartyl proteases can act as beta-secretase proteases useful for
CC treating Alzheimer's disease. APP isoforms are useful for identifying
CC modulators of amyloid-beta peptide production, for use in designing
CC therapeutics for the treatment and prevention of Alzheimer's disease,
CC dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
CC and neuronal loss. APP isoforms are also used in methods for identifying
CC inhibitors and modulators of human Asp2 activity. The invention relates
CC to a method for identifying agents that modulate the activity of human
CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC as a means to screen in cellular assays for the inhibitors of beta- and
CC gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC polymerase chain reactions (PCR). The probes are useful for detecting
CC Hu-Asp nucleic acids in in vitro assays and in Northern and Southern
CC blots. The present cDNA sequence encodes human aspartyl protease 2
CC (Hu-Asp2), a 'long' form designated as (Hu-Asp2a). Hu-Asp 2 gene is
CC localised on chromosome 11q23.3-24.1.

Sequence 2070 BP; 476 A; 583 C; 562 G; 449 T; 0 other;

Query Match 100.0%; Score 2070; DB 22; Length 2070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120

Qy        121 CTGCGGCTGCCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGCGGCTGCCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300

Qy        301 GTGGGTGCTGCCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGGGTGCTGCCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy        421 CTGGGCACCGACCTGGTAAGCATCCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540

Qy        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600

Qy        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660

Qy        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720

Qy        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780

Qy        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840

Qy        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900

Qy        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960

Qy        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020

Qy       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080

Qy       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140

Qy       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200

Qy       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260

Qy       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320

Qy       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380

Qy       1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440

Qy       1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500

Qy       1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560

Qy       1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620

Qy       1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680

Qy       1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740

Qy       1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
```

```
Qy       1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860

Qy       1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920

Qy       1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980

Qy       1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040

Qy       2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
             ||||||||||||||||||||||||||||||
Db       2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
```

RESULT 4
AAS11517
ID AAS11517 standard; cDNA; 2070 BP.
XX
AC AAS11517;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human cDNA encoding Aspartyl protease 2(a), Asp2(a).
XX
KW Human; Aspartyl protease; Asp2(a); beta-secretase; nootropic;
KW neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
KW amyloid-beta; Abeta; ss.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	CDS	1..1506
FT		/*tag= a
FT		/product= "Asp2(a)"
FT	sig_peptide	1..63
FT		/*tag= b
FT	sig_peptide	64..135
FT		/*tag= c
FT		/label= Pre_pro_peptide
FT	sig_peptide	136..171
FT		/*tag= d
FT		/label= Pro_peptide
FT	mat_peptide	172..1503
FT		/*tag= e
FT		/label= Mature_Asp2(a)

XX
PN WO200149098-A2.
XX
PD 12-JUL-2001.
XX
PF 09-MAY-2001; 2001WO-IB00798.
XX
PR 09-MAY-2001; 2001WO-IB00798.
XX
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2001-502549/55.
DR P-PSDB; AAU06603.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity -
XX
PS Claim 98; Fig 2; 185pp; English.
XX
CC The invention relates to a purified polypeptide comprising a fragment of
CC mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
CC transmembrane domain and the Asp2 protein, and where the polypeptide and
CC the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. The invention also details polynucleotides for the Asp
CC proteins and vectors expressing them, and a polypeptide (isoform of
CC amyloid protein precursor (APP)) comprising the amino acid sequence of an
CC APP or its fragment containing an APP cleavage site recognizable by a
CC mammalian beta-secretase, and further comprising two lysine residues at
CC the carboxyl terminus of the amino acid sequence of the mammalian APP or
CC APP fragment. Also included in the invention are methods of identifying
CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
CC useful for treating Alzheimer's disease. APP is useful in methods for
CC identifying inhibitors or modulators of human Asp2 activity and
CC amyloid-beta (Abeta) peptide production. APP is also useful in designing
CC therapeutics for the treatment or prevention of Alzheimer's disease.
CC APP comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which
CC is associated with increased levels of Abeta processing is useful in
CC assays relating the Alzheimer's research. The expression vector is useful
CC for recombinantly expressing APP. Nucleic acids that hybridise to
CC Asp oligonucleotides are useful as probes or primers. The probes are
CC useful for detecting Hu-Asp nucleic acids in in vitro assays and in
CC Northern and Southern blots. The present sequence encodes human Asp2(a).
XX
SQ Sequence 2070 BP; 476 A; 583 C; 562 G; 449 T; 0 other;

Query Match 100.0%; Score 2070; DB 22; Length 2070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120

Qy        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300

Qy        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
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Db        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
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Db        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
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Db        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540

Qy        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
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Db        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
Qy        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
Db        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
Qy        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
Db        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
Qy        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
Db        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
Qy        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
Db        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
          841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
Db        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
Qy        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
Db        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
Qy        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
Db        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
Qy       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
Db       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
Qy       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
Db       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
Qy       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
Db       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
Qy       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
Db       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
Qy       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320
Db       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320
Qy       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
Db       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
Qy       1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440
Db       1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440
Qy       1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
Db       1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
Qy       1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
Db       1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
Qy       1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620
Db       1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620
Qy       1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680
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Db       1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680
Qy       1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740
Db       1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740
Qy       1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
Db       1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
Qy       1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
Db       1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
Qy       1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
Db       1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
Qy       1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
Db       1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
Qy       1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
Db       1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
Qy       2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
Db       2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
```

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RESULT 5
AAS11702
ID   AAS11702 standard; DNA; 2070 BP.
XX
AC   AAS11702;
XX
DT   24-OCT-2001  (first entry)
XX
DE   DNA encoding human aspartyl protease 2a (Asp-2a).
XX
KW   Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;
KW   aspartyl protease 2; Asp2; amyloid protein precursor; APP;
KW   beta-secretase; Alzheimer's disease; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /product= "Aspartyl protease-2a (Asp-2a)"
FT   sig_peptide     1..63
FT                   /*tag=  b
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FT   misc_feature    136..171
FT                   /*tag=  d
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FT   mat_peptide     172..1503
FT                   /*tag=  e
FT                   /note= "Mature Aspartyl protease-2a"
XX
PN   WO200149097-A2.
XX
PD   12-JUL-2001.
XX
PF   09-MAY-2001; 2001WO-IB00797.
XX
PR   09-MAY-2001; 2001WO-IB00797.
XX
PA   (BIEN/) BIENKOWSKI M J.
PA   (GURN/) GURNEY M E.
```

PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2001-502548/55.
DR P-PSDB; AAU07102.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity -
XX
PS Claim 98; Fig 2; 185pp; English.
XX
CC The invention relates to a novel purified polypeptide comprising a
CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
CC and the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. Also included is an isoform of amyloid protein precursor (APP)
CC comprising the amino acid sequence of a APP or its fragment containing
CC an APP cleavage site recognisable by a mammalian beta-secretase, and
CC further comprising two lysine residues at the carboxyl terminus of the
CC amino acid sequence of the mammalian APP or APP fragment. The
CC polypeptides are used for assaying for modulators of beta-secretase
CC activity; identifying agents that inhibit the APP processing activity
CC of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that
CC modulate the activity of Asp2; and for reducing cellular production of
CC amyloid beta (Abeta) from APP. Agents identified by the above methods
CC are useful for treating Alzheimer's disease; and for identifying
CC modulators of amyloid-beta (Abeta) peptide production, for use in
CC designing therapeutics for the treatment or prevention of Alzheimer's
CC disease. Probes and primers derived from Asp nucleic acid sequences
CC are useful for detecting Hu-Asp nucleic acids in in vitro assays and in
CC Northern and Southern blots. The present sequence represents the
CC coding sequence of human Asp-2a used in the methods of the invention.
XX
SQ Sequence 2070 BP; 476 A; 583 C; 562 G; 449 T; 0 other;

Query Match 100.0%; Score 2070; DB 22; Length 2070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

           61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGGCGCCCCCCTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
           61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120

Qy        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300

Qy        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
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Db        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
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Db        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540

Qy        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600

Qy        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
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Db        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660

Qy        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720

Qy        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780

Qy        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840

Qy        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900

Qy        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020

Qy       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080

Qy       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140

Qy       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200

Qy       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260

Qy       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320

Qy       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380

Qy       1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440

Qy       1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500

Qy       1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560

Qy       1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620

Qy       1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680

Qy       1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740

Qy       1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800

Qy       1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860

Qy       1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920

Qy       1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980

Qy       1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040

Qy       2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
             ||||||||||||||||||||||||||||||
Db       2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
```

RESULT 6
AAD06739
ID AAD06739 standard; cDNA; 2070 BP.
XX
AC AAD06739;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human aspartyl protease 2a (Asp2a) cDNA.
XX
KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;
KW Alzheimer's disease; antialzheimer's; aspartyl protease 2a; Asp 2a;
KW beta-secretase; chromosome 11q23.3-24.1; ss.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	CDS	1..1506
FT		/*tag= a
FT		/product= "Human aspartyl protease 2a"
FT	sig_peptide	1..63
FT		/*tag= b
FT	sig_peptide	64..135
FT		/*tag= c
FT		/note= "Pre-pro-peptide"
FT	sig_peptide	136..171
FT		/*tag= d
FT		/note= "Pro-peptide"
FT	mat_peptide	172..1503
FT		/*tag= e
FT		/product= "Human mature aspartyl protease 2a"

XX
PN WO200123533-A2.
XX
PD 05-APR-2001.
XX
PF 22-SEP-2000; 2000WO-US26080.
XX
PR 23-SEP-1999; 99US-0155493.
PR 23-SEP-1999; 99WO-US20881.
PR 13-OCT-1999; 99US-0416901.
PR 06-DEC-1999; 99US-0169232.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Gurney M, Bienkowski MJ;
XX
DR WPI; 2001-290516/30.
DR P-PSDB; AAE02581.
XX
PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT protein, useful for the treatment of Alzheimer's disease -
XX
PS Example 2; Page 126-127; 189pp; English.
XX
CC The present invention relates to enzymes for cleaving the alpha-
CC secretase site of the amyloid precursor protein (APP) and methods of
CC identifying those enzymes. The methods may be used to identify enzymes
CC that may be used to cleave the alpha-secretase cleavage site of the APP
CC protein. The enzymes may be used to treat or modulate the progress of
CC Alzheimer's disease. The present sequence is human aspartyl protease
CC (Asp) 2a cDNA. Asp 2a has beta-secretase protease activity. Asp2 gene
CC is located on chromosome 11q23.3-24.1.
XX
SQ Sequence 2070 BP; 476 A; 583 C; 562 G; 449 T; 0 other;

Query Match 100.0%; Score 2070; DB 22; Length 2070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120

Qy        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
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Db        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
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Db        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy        241 GTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
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Db        241 GTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300

Qy        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
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Db        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
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Qy        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
```

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Db        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600

Qy        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
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Db        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660

Qy        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720

Qy        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780

Qy        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840

Qy        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900

Qy        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
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Db        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960

Qy        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
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Db        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020

Qy       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
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Db       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080

Qy       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140

Qy       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200

Qy       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
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Db       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260

Qy       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320

Qy       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380

Qy       1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440

Qy       1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
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Db       1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500

Qy       1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
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Db       1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560

Qy       1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620
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Db       1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620

Qy       1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680

Qy       1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740

Qy       1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800

Qy       1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
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Db       1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860

Qy       1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
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Db       1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920

Qy       1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980

Qy       1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040

Qy       2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
              ||||||||||||||||||||||||||||||
Db       2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
```

RESULT 7
ABL52457
ID ABL52457 standard; cDNA; 2070 BP.
XX
AC ABL52457;
XX
DT 16-JUL-2002 (first entry)
XX
DE Human Asp-2(a) nucleotide sequence SEQ ID NO:3.
XX
KW Human; Asp-1; Asp-2; aspartyl protease; enzyme; Alzheimer's disease;
KW proteolytic; chromosome 11q23.3-24.1; gene; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1..1506
FT   /*tag= a
FT   /product= "Asp-2(a)"
FT   /note= "aspartyl protease"
XX
PN GB2367060-A.
XX
PD 27-MAR-2002.
XX
PF 29-OCT-2001; 2001GB-0025934.
XX
PR 23-SEP-1999; 99US-155493P.
PR 23-SEP-1999; 99US-0404133.
PR 23-SEP-1999; 99WO-US20881.
PR 13-OCT-1999; 99US-0416901.
PR 06-DEC-1999; 99US-169232P.
PR 22-SEP-2000; 2000GB-0023315.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Bienkowkski MJ, Gurney M;
XX
DR WPI; 2002-396337/43.
DR P-PSDB; ABB78590.
XX
PT Human aspartyl protease 1 substrates useful in assays to detect

PT aspartyl protease activity, e.g. for the diagnosis of Alzheimer's
PT disease -
XX
PS Example 2; Fig 2; 182pp; English.
XX
CC The present invention describes a human aspartyl protease 1 (hu-Asp1)
CC substrate (I) which comprises a peptide of no more than 50 amino acids,
CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
CC (I) under acidic conditions; and (b) determining the level of hu-Asp1
CC proteolytic activity; (2) a purified polynucleotide (III) comprising a
CC nucleotide sequence that hybridises under stringent conditions to the
CC non-coding strand complementary to a defined 1804 nucleotide sequence
CC (see ABL52456) where the nucleotide sequence encodes a polypeptide having
CC Asp1 proteolytic activity and lacks nucleotides encoding a transmembrane
CC domain); (3) a purified polynucleotide (III') comprising a sequence that
CC hybridises under stringent conditions to (III) (the nucleotide sequence
CC encodes a polypeptide further lacking a pro-peptide domain corresponding
CC to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)
CC comprising (III) or (III'); and (5) a host cell (V) transformed or
CC transfected with (III), (III') and/or (IV). The hu-Asp1 protease
CC substrate (I) may be used as an enzyme substrate in assays to detect
CC aspartyl protease activity, (II) and therefore diagnose diseases
CC associated with aberrant hu-Asp1 expression and activity such as
CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
CC sequence encodes hu-Asp2(a) from the present invention.
XX
SQ Sequence 2070 BP; 476 A; 583 C; 562 G; 449 T; 0 other;

Query Match 100.0%; Score 2070; DB 24; Length 2070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120

Qy        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
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Db        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300

Qy        301 GTGGGTGCTGCCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
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Db        301 GTGGGTGCTGCCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540

Qy        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600

Qy        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660

Qy        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720

Qy        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780

Qy        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840

Qy        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900

Qy        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960

Qy        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020

Qy       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080

Qy       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140

Qy       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200

Qy       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260

Qy       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320

Qy       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380

Qy       1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440

Qy       1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500

Qy       1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560

Qy       1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620

Qy       1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680
```

```
Qy       1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740

Qy       1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800

Qy       1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860

Qy       1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920

Qy       1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980

Qy       1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040

Qy       2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
             |||||||||||||||||||||||||||||||
Db       2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
```

RESULT 8
ABL49914
ID ABL49914 standard; DNA; 2070 BP.
XX
AC ABL49914;
XX
DT 31-MAY-2002 (first entry)
XX
DE Human aspartyl protease nucleotide sequence SEQ ID NO:1.
XX
KW Beta-secretase; enzyme; cleavage site; amyloid protein precursor; APP;
KW aspartyl protease; neuroprotective; nootropic; beta-secretase inhibitor;
KW Alzheimer's disease; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200206306-A2.
XX
[redacted] 24-JAN-2002.
[redacted]
[redacted] 19-JUL-2001; 2001WO-US23035.
XX
PR 19-JUL-2000; 2000US-219795P.
PR 12-MAR-2001; 2001US-275251P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Yan R, Tomasselli AG, Gurney ME, Emmons TL, Bienkowski MJ;
PI Heinrikson RL;
XX
DR WPI; 2002-216995/27.
DR P-PSDB; ABB06409.
XX
PT Novel substrates for human aspartyl protease useful for identifying
PT modulators of beta secretase activity of aspartyl protease for treating
PT Alzheimer's disease -
XX
PS Claim 1; Page 117; 188pp; English.
XX
CC The present invention describes an isolated peptide (I) comprising a
CC sequence of at least four amino acids, where the peptide is a substrate
CC for conducting aspartyl protease assays. (I) has neuroprotective and
CC nootropic activities, and can be used as an inhibitor of beta-secretase
CC activity. A beta-secretase modulator from the present invention can be
CC used for inhibiting beta-secretase activity in vivo, and in the
CC manufacture of a medicament for the treatment of Alzheimer's disease.
CC Pharmaceutical compositions from the present invention can be used for
CC treating a disease or condition characterised by an abnormal beta-
CC secretase activity. (I) is useful for identifying agents that modulate
CC the activity of human Asp2 aspartyl protease (Hu-Asp2). (I) is useful
CC as a core structure to construct derivatives. ABL49914 to ABL49925 and
CC ABB06409 to ABB06593 represent sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 2070 BP; 476 A; 583 C; 562 G; 449 T; 0 other;

```
  Query Match            100.0%;  Score 2070;  DB 24;  Length 2070;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2070;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120

Qy        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300

Qy        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540

Qy        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600

Qy        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660

Qy        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720

Qy        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780

Qy        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
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Qy       841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900

Qy       901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960

Qy       961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020

Qy      1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080

Qy      1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140

Qy      1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200

Qy      1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260

Qy      1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320

Qy      1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380

Qy      1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440

Qy      1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500

Qy      1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560

Qy      1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620

Qy      1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680

Qy      1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740

Qy      1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800

Qy      1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860

Qy      1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920

Qy      1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980

Qy      1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040

Qy      2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
            ||||||||||||||||||||||||||||||
Db      2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
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RESULT 9
AAA59553
ID AAA59553 standard; DNA; 16080 BP.
XX
AC AAA59553;
XX
DT 14-NOV-2000 (first entry)
XX
DE DNA clone pCEK C1.27 encoding a human beta-secretase enzyme.
XX
KW Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
KW amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
KW inhibitor; ss.
XX
OS Homo sapiens.
XX
PN WO200047618-A2.
XX
PD 17-AUG-2000.
XX
PF 10-FEB-2000; 2000WO-US03819.
XX
PR 10-FEB-1999; 99US-0119571.
PR 15-JUN-1999; 99US-0139172.
XX
PA (ELAN-) ELAN PHARM INC.
XX
PI Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;
PI Sinha S, Tatsuno G, Tung J, Wang S, McConlogue L;
XX
DR WPI; 2000-533011/48.
XX
PT Purified beta-secretase protein used in assays to discover inhibitors
PT which can be used for the treatment of amyloidogenic diseases e.g.
PT Alzheimer's disease -
XX
PS Disclosure; Fig 13A-E; 121pp; English.
XX
CC The specification describes a beta-secretase enzyme. The enzyme cleaves
CC beta-amyloid precursor protein to produce beta-amyloid peptide. This
CC enzyme is therefore implicated in the production of amyloid plaque
CC components which accumulate in the brains of individuals afflicted with
CC Alzheimer's disease. Inhibitors of beta-secretase are administered to
CC a mammalian subject e.g. with Alzheimer's disease or Alzheimer's
CC disease-like pathology to test if they maintain or improve cognitive
CC ability or reduce the plaque burden. The compounds are used for the
CC treatment of amyloidogenic diseases e.g. Alzheimer's disease. The
CC present sequence encodes a human beta-secretase enzyme.
XX
SQ Sequence 16080 BP; 3627 A; 4556 C; 3962 G; 3913 T; 22 other;

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  Query Match            98.9%;  Score 2047.8;  DB 21;  Length 16080;
  Best Local Similarity  99.7%;  Pred. No. 0;
  Matches 2052;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1675 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 1734

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1735 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 1794

Qy        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1795 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 1854

Qy        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1855 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 1914

Qy        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1915 GTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 1974

Qy        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1975 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 2034

Qy        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2035 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 2094

Qy        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2095 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 2154

Qy        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2155 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 2214

Qy        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2215 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 2274

Qy        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       2275 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGCTTC 2334

Qy        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2335 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 2394

Qy        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2395 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 2454

Qy        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          2455 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 2514

             841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2515 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 2574

Qy        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2575 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 2634

Qy        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2635 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 2694

Qy       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2695 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 2754

Qy       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2755 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 2814

Qy       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       2815 TACAAGTTTGCCATCTCACAGTCATCCACGCGCACTGTTATGGGAGCTGTTATCATGGAG 2874
```

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Qy       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2875 GCCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 2934

Qy       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2935 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 2994

Qy       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2995 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 3054

Qy       1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3055 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 3114

Qy       1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3115 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 3174

Qy       1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db       3175 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTCGTTCA 3234

Qy       1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3235 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 3294

Qy       1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3295 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 3354

Qy       1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3355 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 3414

Qy       1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3415 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 3474

Qy       1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3475 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 3534

Qy       1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3535 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 3594

Qy       1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3595 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 3654

Qy       1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3655 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 3714

Qy       2041 ATTAAAAAAAAAAAAAAAA 2059
              ||||||||||||||  | |
Db       3715 ATTAAAAAAAAAAACTAGA 3733
```

```
RESULT 10
AAA59551
ID   AAA59551 standard; DNA; 2348 BP.
XX
AC   AAA59551;
XX
DT   14-NOV-2000  (first entry)
XX
DE   DNA encoding a human beta-secretase enzyme.
XX
KW   Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
```

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KW   amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
KW   inhibitor; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             306..1811
FT                   /*tag= a
FT                   /product= "beta-secretase"
XX
PN   WO200047618-A2.
XX
PD   17-AUG-2000.
XX
PF   10-FEB-2000; 2000WO-US03819.
XX
PR   10-FEB-1999;   99US-0119571.
PR   15-JUN-1999;   99US-0139172.
XX
PA   (ELAN-) ELAN PHARM INC.
XX
PI   Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;
PI   Sinha S, Tatsuno G, Tung J, Wang S, McConlogue L;
XX
DR   WPI; 2000-533011/48.
DR   P-PSDB; AAB07896.
XX
PT   Purified beta-secretase protein used in assays to discover inhibitors
PT   which can be used for the treatment of amyloidogenic diseases e.g.
PT   Alzheimer's disease -
XX
PS   Disclosure; Fig 1B; 121pp; English.
XX
CC   The specification describes a beta-secretase enzyme. The enzyme cleaves
CC   beta-amyloid precursor protein to produce beta-amyloid peptide. This
CC   enzyme is therefore implicated in the production of amyloid plaque
CC   components which accumulate in the brains of individuals afflicted with
CC   Alzheimer's disease. Inhibitors of beta-secretase are administered to
CC   a mammalian subject e.g. with Alzheimer's disease or Alzheimer's
CC   disease-like pathology to test if they maintain or improve cognitive
CC   ability or reduce the plaque burden. The compounds are used for the
CC   treatment of amyloidogenic diseases e.g. Alzheimer's disease. The
CC   present sequence encodes a human beta-secretase enzyme.
XX
SQ   Sequence 2348 BP; 489 A; 713 C; 661 G; 484 T; 1 other;

  Query Match             98.5%;  Score 2039.8;  DB 21;  Length 2348;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2041;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 365

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 425

Qy        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 485

Qy        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 545

Qy        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 605

Qy        301 GTGGGTGCTGCCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 GTGGGTGCTGCCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 665

Qy        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 725

Qy        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 785

Qy        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 845

Qy        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 905

Qy        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        906 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGCTTC 965

Qy        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 1025

Qy        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 1085

Qy        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1086 GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 1145

Qy        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1146 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 1205

Qy        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1206 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 1265

Qy        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1266 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1325

Qy       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1326 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1385

Qy       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1386 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1445

Qy       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1446 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1505

Qy       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1506 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1565

Qy       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1566 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1625

Qy       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1626 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1685

Qy       1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1686 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1745
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Qy       1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1746 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1805

Qy       1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1806 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1865

Qy       1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1866 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1925

Qy       1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1926 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1985

Qy       1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1986 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 2045

Qy       1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2046 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 2105

Qy       1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2106 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 2165

Qy       1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2166 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 2225

Qy       1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2226 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 2285

Qy       1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2286 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2345

Qy       2041 ATT 2043
             |||
Db       2346 ATT 2348


RESULT 11
AAV41696
ID   AAV41696 standard; cDNA; 2541 BP.
XX
AC   AAV41696;
XX
DT   26-OCT-1998  (first entry)
XX
DE   Nucleotide sequence of human ASP2 (aspartic protease 2).
XX
KW   Human; ASP2; aspartic protease 2; agonist; antagonist; immunospecific;
KW   antibody; inhibition; Alzheimer's disease; cancer; proteinase;
KW   prohormone processing; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1506
FT                   /*tag=  a
FT                   /product= "human ASP2"
XX
PN   EP855444-A2.
XX
PD   29-JUL-1998.
XX
PF   27-JAN-1998;   98EP-0300573.
XX
PR   28-JAN-1997;   97GB-0001684.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Chapman CG,  Murphy K,  Powell DJ,  Smith TS;
XX
DR   WPI; 1998-389809/34.
DR   P-PSDB; AAW59807.
XX
PT   New nucleic acid encoding human aspartic protease 2 - used to treat,
PT   prevent and diagnose e.g. Alzheimer's disease, cancer and prohormone
PT   processing
XX
PS   Claim 2; Pages 6-7; 26pp; English.
XX
CC   This is the nucleotide sequence of the human ASP2 (aspartic protease 2),
CC   used in the method of the invention.  Agonists and antagonists for
CC   ASP2 immunospecific antibodies are used to treat conditions requiring
CC   increased or decreased activity or expression of ASP2 respectively.
CC   ASP2 is used to treat and diagnose e.g. Alzheimer's disease, cancer
CC   and prohormone processing and ASP2 or a fragment can be used to induce
CC   an immune response against the above conditions.
XX
SQ   Sequence 2541 BP; 598 A; 673 C; 675 G; 579 T; 16 other;

  Query Match             98.2%;  Score 2032;  DB 19;  Length 2541;
  Best Local Similarity   99.5%;  Pred. No. 0;
  Matches 2049;  Conservative    0;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120

Qy        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300

Qy        301 GTGGGTGCTGCCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGGGTGCTGCCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        361 TACCGGGACCTCCGGAAGGGTGTGTATGAGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540

Qy        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600

Qy        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGCTTC 660
```

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Qy       661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720

Qy       721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780

Qy       781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
            ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840

Qy       841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900

Qy       901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960

Qy       961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020

Qy      1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080

Qy      1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140

Qy      1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200

Qy      1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260

Qy      1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320

Qy      1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380

y       1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440

Qy      1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500

Qy      1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT-GGACCACACCTCCGTGGTTC 1559
            |||||||||||||||||  ||||||||||||||||| ||||||||||||||||||||||||
Db      1501 AAGTGAGGAGGCCCATGGGAGAAAGATAGAGATTCCCCTGGGACCACACCTCCGTGGTTC 1560

Qy      1560 ACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTC 1619
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1561 ACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTC 1620

Qy      1620 CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCA 1679
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1621 CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCA 1680

Qy      1680 GGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATAC 1739
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681 GGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATAC 1740

Qy      1740 TCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACC 1799
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741 TCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACC 1800

Qy      1800 TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGA 1859
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1801 TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGA 1860

Qy      1860 AGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAA 1919
            |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db      1861 AGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCGGGCAGAGAA 1920

Qy      1920 GAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTAT 1979
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1921 GAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTAT 1980

Qy      1980 TTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTG 2039
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1981 TTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTG 2040

Qy      2040 AATTAAAAAAAAAAAAAAAA 2059
            |||||||||||||||  | |
Db      2041 AATTAAAAAAAAAAACTAGA 2060
```

RESULT 12
AAF31848
ID AAF31848 standard; cDNA; 3252 BP.
XX
AC AAF31848;
XX
DT 12-APR-2001 (first entry)
XX
DE Human memapsin 2 cDNA.
XX
KW Human; memapsin 2; nootropic; neuroprotective; amyloid precursor protein;
KW APP; memapsin 2 inhibitor; Alzheimer's disease; ds.
XX
OS Homo sapiens.
XX
PN WO200100665-A2.
XX
PD 04-JAN-2001.
XX
PF 27-JUN-2000; 2000WO-US17742.
XX
PR 28-JUN-1999; 99US-0141363.
PR 30-NOV-1999; 99US-0168060.
PR 25-JAN-2000; 2000US-0177836.
PR 27-JAN-2000; 2000US-0178368.
PR 08-JUN-2000; 2000US-0210292.
XX
PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
PA (UNII) UNIV ILLINOIS FOUND.
XX
PI Tang JJN, Hong L, Ghosh AK;
XX
DR WPI; 2001-137933/14.
DR P-PSDB; AAB66572.
XX
PT Novel memapsin 2 inhibitors which bind to active site of memapsin 2
PT having 2 catalytic aspartic residues and substrate binding cleft, used
PT to treat Alzheimer's disease by blocking amyloid precursor protein
PT cleavage -
XX
PS Example 1; Page 70-71; 86pp; English.
XX
CC The present sequence is given in a specification relating to an inhibitor
CC of catalytically active memapsin 2. The inhibitor binds to the memapsin 2
CC active site, which is defined by the presence of two catalytic aspartic
CC residues and a substrate binding cleft. The inhibitor is useful for
CC the treatment and diagnosis of Alzheimer's disease. It is useful in
CC screens for individuals with a genetic predisposition to Alzheimer's
CC disease. The inhibitor is useful as a reagent for specifically binding to

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CC   memapsin 2 or memapsin 2 analogues and for aiding in memapsin 2
CC   isolation, purification and characterisation.
XX
SQ   Sequence 3252 BP; 804 A; 863 C; 811 G; 771 T; 3 other;

  Query Match             97.1%;  Score 2010;  DB 22;  Length 3252;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 2013;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         40 GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC  99
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC  60

Qy        100 CTGGGGGGGCGCCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAG 159
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTGGGGGGGCGCCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAG 120

Qy        160 CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 180

Qy        220 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 279
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 240

Qy        280 ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTAC 339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTAC 300

Qy        340 CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC 399
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC 360

Qy        400 CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC 459
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC 420

Qy        460 GTCACTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC 519
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTCACTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC 480

Qy        520 TCCAACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC 579
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC 540

Qy        580 CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG 639
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG 600

Qy        640 CACCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGG 699
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGG 660

Qy        700 AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC 759
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC 720

Qy        760 ATCCGGCGGGAGTGGTATTATGAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGAT 819
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        721 ATCCGGCGGGAGTGGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGAT 780

Qy        820 CTGAAAATGGACTGCAAGGAGTACAACTATGACAAGAGCATTGTGGACAGTGGCACCACC 879
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CTGAAAATGGACTGCAAGGAGTACAACTATGACAAGAGCATTGTGGACAGTGGCACCACC 840

Qy        880 AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC 939
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC 900

Qy        940 TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA 999
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA 960

Qy       1000 GGCACCACCCCTTGGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC 1059
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GGCACCACCCCTTGGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC 1020

Qy       1060 AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG 1119
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG 1080

Qy       1120 GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT 1179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT 1140

Qy       1180 ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT 1239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT 1200

Qy       1240 GGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC 1299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC 1260

Qy       1300 CCTTTTGTCACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA 1359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CCTTTTGTCACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA 1320

Qy       1360 ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC 1419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC 1380

Qy       1420 TGCCTCATGGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT 1479
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TGCCTCATGGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT 1440

Qy       1480 GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT 1539
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT 1500

Qy       1540 GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC 1599
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC 1560

Qy       1600 CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA 1659
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA 1620

Qy       1660 GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG 1719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG 1680

Qy       1720 CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT 1779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT 1740

Qy       1780 TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATT 1839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATT 1800

Qy       1840 CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCC 1899
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCC 1860

Qy       1900 TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA 1959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA 1920

Qy       1960 GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT 2019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT 1980

Qy       2020 GGTGCAAAGATTGCCTCTTGAATTAAAAAAAAAAAAAA 2057
              |||||||||||||||||||||||||||||||||||  | |
Db       1981 GGTGCAAAGATTGCCTCTTGAATTAAAAAAAAACTAGA 2018
```

RESULT 13
AAF28101
ID AAF28101 standard; DNA; 3252 BP.
XX
AC AAF28101;
XX
DT 02-APR-2001 (first entry)
XX
DE Memapsin 2 DNA.
XX
KW Memapsin 2; catalyst; Alzheimer's; ds.
XX
OS Homo sapiens.
XX
PN WO200100663-A2.
XX
PD 04-JAN-2001.
XX
PF 27-JUN-2000; 2000WO-US17661.
XX
PR 28-JUN-1999; 99US-0141363.
PR 30-NOV-1999; 99US-0168060.
PR 25-JAN-2000; 2000US-0177836.
PR 27-JAN-2000; 2000US-0178368.
PR 08-JUN-2000; 2000US-0210292.
XX
PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX
PI Tang JJN, Lin X, Koelsch G;
XX
DR WPI; 2001-102885/11.
XX
PT Purified recombinant catalytically active memapsin 2, used to screen
PT inhibitors of it, which are used to treat and prevent Alzheimer's
PT disease -
XX
PS Example 1; Page 71-72; 86pp; English.
XX
CC The present invention relates to a purified recombinant
CC catalytically active memapsin 2. The invention may be used for
CC isolating inhibitors which are used to treat or prevent
CC Alzheimer's disease. The invention may also be used to screen
CC for individuals more genetically prone to develop Alzheimer's
CC disease.
XX
SQ Sequence 3252 BP; 804 A; 863 C; 811 G; 771 T; 3 other;

Query Match 97.1%; Score 2010; DB 22; Length 3252;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2013; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy        40 GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC 99
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC 60

Qy       100 CTGGGGGGCGCCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAG 159
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 CTGGGGGGCGCCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAG 120

Qy       160 CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 219
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 180

Qy       220 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 279
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 240

Qy       280 ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTAC 339
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTAC 300

Qy       340 CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC 399
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC 360

Qy       400 CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC 459
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC 420

Qy       460 GTCACTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC 519
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 GTCACTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC 480

Qy       520 TCCAACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC 579
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 TCCAACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC 540

Qy       580 CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG 639
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG 600

Qy       640 CACCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGG 699
             || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 CAGCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGG 660

Qy       700 AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC 759
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC 720

Qy       760 ATCCGGCGGGAGTGGTATTATGAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGAT 819
             |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       721 ATCCGGCGGGAGTGGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGAT 780

Qy       820 CTGAAAATGGACTGCAAGGAGTACAACTATGACAAGAGCATTGTGGACAGTGGCACCACC 879
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 CTGAAAATGGACTGCAAGGAGTACAACTATGACAAGAGCATTGTGGACAGTGGCACCACC 840

Qy       880 AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC 939
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC 900

Qy       940 TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA 999
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA 960

Qy      1000 GGCACCACCCCTTGGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC 1059
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 GGCACCACCCCTTGGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC 1020

Qy      1060 AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG 1119
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG 1080

Qy      1120 GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT 1179
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT 1140

Qy      1180 ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT 1239
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT 1200

Qy      1240 GGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC 1299
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 GGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC 1260

Qy      1300 CCTTTTGTCACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA 1359
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 CCTTTTGTCACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA 1320

Qy      1360 ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC 1419
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC 1380

Qy      1420 TGCCTCATGGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT 1479
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 TGCCTCATGGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT 1440
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Qy       1480 GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT 1539
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT 1500

Qy       1540 GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC 1599
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC 1560

Qy       1600 CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA 1659
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA 1620

Qy       1660 GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG 1719
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG 1680

Qy       1720 CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT 1779
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT 1740

Qy       1780 TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATT 1839
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATT 1800

Qy       1840 CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCC 1899
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCC 1860

Qy       1900 TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA 1959
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA 1920

Qy       1960 GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT 2019
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT 1980

Qy       2020 GGTGCAAAGATTGCCTCTTGAATTAAAAAAAAAAAAAA 2057
             ||||||||||||||||||||||||||||||||  | |
Db       1981 GGTGCAAAGATTGCCTCTTGAATTAAAAAAAAACTAGA 2018
```

RESULT 14
ABK88641
ID ABK88641 standard; cDNA; 3252 BP.
XX
AC ABK88641;
XX
    07-OCT-2002 (first entry)

    cDNA encoding human memapsin 2.
XX
KW Human; memapsin 2; beta secretase; aspartic protease; APP;
KW beta-amyloid precursor protein; amyloid plaque; Alzheimer's disease;
KW neuroprotective; nootropic; expressed sequence tag; EST; gene; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1..1467
FT   /*tag= a
FT   /partial
FT   /product= "Memapsin 2"
FT   /note= "This sequence lacks a start codon"
XX
PN US2002049303-A1.
XX
PD 25-APR-2002.
XX
PF 28-FEB-2001; 2001US-0796264.
XX
PR 28-JUN-1999; 99US-141363P.
PR 30-NOV-1999; 99US-168060P.
PR 25-JAN-2000; 2000US-177836P.
PR 27-JAN-2000; 2000US-178368P.
PR 27-JUN-2000; 2000US-0604608.
XX
PA (TANG/) TANG J J N.
PA (LINX/) LIN X.
PA (KOEL/) KOELSCH G.
PA (HONG/) HONG L.
XX
PI Tang JJN, Lin X, Koelsch G, Hong L;
XX
DR WPI; 2002-507280/54.
DR P-PSDB; AAU99488.
XX
PT New recombinant catalytically active memapsin 2, useful to screen for
PT inhibitors of memapsin 2 which can be used to prevent and treat
PT Alzheimer's disease
XX
PS Example 1; Page 20-21; 44pp; English.
XX
CC The present invention relates to methods for the production of
CC purified, recombinant catalytically active, memapsin 2 (beta
CC secretase). Memapsin 2, a member of the aspartic protease family,
CC cleaves beta-amyloid precursor protein (APP) found in amyloid plaques.
CC The recombinant memapsin 2 is useful for identifying inhibitors of
CC memapsin 2 in the design of drugs for the treatment and/or prevention
CC of Alzheimer's disease. The recombinant memapsin 2 can be used to
CC immunise against Alzheimer's disease. The present sequence encodes
CC human memapsin 2.
XX
SQ Sequence 3252 BP; 804 A; 863 C; 811 G; 771 T; 3 other;

Query Match 97.1%; Score 2010; DB 24; Length 3252;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2013; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy         40 GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC 99
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC 60

Qy        100 CTGGGGGGCGCCCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAG 159
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTGGGGGGCGCCCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAG 120

Qy        160 CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 180

Qy        220 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 279
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 240

Qy        280 ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTAC 339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTAC 300

Qy        340 CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC 399
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC 360

Qy        400 CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC 459
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC 420

Qy        460 GTCACTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC 519
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTCACTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC 480

Qy        520 TCCAACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC 579
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC 540

Qy        580 CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG 639
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Db        541 CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG 600
Qy        640 CACCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGG 699
Db        601 CAGCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGG 660
Qy        700 AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC 759
Db        661 AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC 720
Qy        760 ATCCGGCGGGAGTGGTATTATGAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGAT 819
Db        721 ATCCGGCGGGAGTGGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGAT 780
Qy        820 CTGAAAATGGACTGCAAGGAGTACAACTATGACAAGAGCATTGTGGACAGTGGCACCACC 879
Db        781 CTGAAAATGGACTGCAAGGAGTACAACTATGACAAGAGCATTGTGGACAGTGGCACCACC 840
Qy        880 AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC 939
Db        841 AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC 900
Qy        940 TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA 999
Db        901 TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA 960
Qy       1000 GGCACCACCCCTTGGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC 1059
Db        961 GGCACCACCCCTTGGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC 1020
Qy       1060 AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG 1119
Db       1021 AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG 1080
Qy       1120 GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT 1179
Db       1081 GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT 1140
Qy       1180 ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT 1239
Db       1141 ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT 1200
Qy       1240 GGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC 1299
Db       1201 GGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC 1260
Qy       1300 CCTTTTGTCACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA 1359
Db       1261 CCTTTTGTCACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA 1320
Qy       1360 ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC 1419
Db       1321 ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC 1380
Qy       1420 TGCCTCATGGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT 1479
Db       1381 TGCCTCATGGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT 1440
Qy       1480 GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT 1539
Db       1441 GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT 1500
Qy       1540 GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC 1599
Db       1501 GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC 1560
Qy       1600 CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA 1659
Db       1561 CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA 1620
Qy       1660 GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG 1719
Db       1621 GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG 1680
Qy       1720 CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT 1779
Db       1681 CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT 1740
Qy       1780 TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATT 1839
Db       1741 TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATT 1800
Qy       1840 CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCC 1899
Db       1801 CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCC 1860
Qy       1900 TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA 1959
Db       1861 TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA 1920
Qy       1960 GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT 2019
Db       1921 GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT 1980
Qy       2020 GGTGCAAAGATTGCCTCTTGAATTAAAAAAAAAAAAAA 2057
Db       1981 GGTGCAAAGATTGCCTCTTGAATTAAAAAAAAACTAGA 2018
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RESULT 15
ABL39774
ID ABL39774 standard; cDNA; 5757 BP.
XX
AC ABL39774;
XX
DT 10-MAY-2002 (first entry)
XX
DE Human NS cDNA sequence SEQ ID NO:84.
XX
KW Human; cytostatic; osteopathic; gynaecological; neuroprotective;
KW antirheumatic; antiarthritic; antipsoriatic; ophthalmological; anti-HIV;
KW vasotropic; antiarteriosclerotic; antiinflammatory; dermatological;
KW anorectic; muscular; antiinfertility; cardiovascular; anticoagulant;
KW antifibrinolytic; hypotension; antiasthmatic; immunomodulator; cardiant;
KW anticonvulsant; antidiabetic; tranquilliser; antidepressant; aeuroleptic;
KW gastrointestinal; virucide; antiulcer; cerebroprotective; nootropic;
KW contraceptive; vaccine; gene therapy; cancer; osteoporosis; dystonia;
KW endometriosis; degenerative disease; multiple sclerosis; psoriasis;
KW rheumatoid arthritis; cataract; restenosis; atherosclerosis; glaucoma;
KW inflammation; skin disorder; obesity; muscular dystrophy; AIDS;
KW infertility; cardiovascular disease; coagulation disease; hypertension;
KW ischaemia; asthma; immune disease; epilepsy; angina; neurodegeneration;
KW diabetes; anxiety; depression; schizophrenia; viral disease; stroke;
KW gastric ulcer; Alzheimer's disease; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200206315-A2.
XX
PD 24-JAN-2002.
XX
PF 17-JUL-2001; 2001WO-IL00653.
XX
PR 18-JUL-2000; 2000IL-0137345.
PR 15-DEC-2000; 2000IL-0140354.
XX
PA (COMP-) COMPUGEN LTD.
XX
PI Mintz L, Freilich S, Bernstein J;
XX
DR WPI; 2002-155037/20.
DR P-PSDB; ABB06120.
XX
PT One hundred and twenty eight novel nucleic acid sequences, useful for
PT treating and diagnosing e.g. cancer, asthma and Alzheimer's -

XX
PS Claim 1; Page 124-126; 290pp; English.
XX
CC ABL39691 to ABL39818 represent novel human nucleic acid sequences
CC encoding the proteins given in ABB06037 to ABB06164. The novel sequences
CC (NS) can have cytostatic, osteopathic, gynaecological, neuroprotective,
CC antirheumatic, antiarthritic, antipsoriatic, ophthalmological, virucide,
CC vasotropic, antiarteriosclerotic, antiinflammatory, dermatological,
CC anorectic, muscular, anti-HIV, antiinfertility, cardiovascular,
CC anticoagulant, antifibrinolytic, hypotension, antiasthmatic, cardiant,
CC immunomodulator, anticonvulsant, antidiabetic, tranquilliser, antiulcer,
CC antidepressant, gastrointestinal, aeuroleptic, cerebroprotective,
CC nootropic and contraceptive activities. The NS can be used in vaccines,
CC gene therapy and antisense therapy. Nucleic acids, expression vectors and
CC antibodies from the present invention can be used for treating and
CC diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative
CC diseases, dystonia, multiple sclerosis, rheumatoid arthritis, psoriasis,
CC cataracts, restenosis, atherosclerosis, inflammation, skin disorders,
CC glaucoma, obesity, muscular dystrophy, AIDS, infertility, cardiovascular
CC disease, coagulation disease, ischaemia, hypertension, asthma, immune
CC disease, epilepsy, angina, neurodegeneration, diabetes, anxiety,
CC depression, schizophrenia, viral disease, gastric ulcers, stroke,
CC Alzheimer's disease and as a contraceptive.
XX
SQ Sequence 5757 BP; 1485 A; 1490 C; 1392 G; 1388 T; 2 other;

Query Match 91.5%; Score 1894.2; DB 24; Length 5757;
Best Local Similarity 96.2%; Pred. No. 0;
Matches 1981; Conservative 0; Mismatches 3; Indels 75; Gaps 1;

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Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        455 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 514

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        515 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 574

Qy        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        575 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 634

Qy        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        635 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 694

Qy        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        695 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 754

Qy        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        755 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 814

Qy        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        815 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 874

Qy        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        875 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 934

Qy        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        935 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 994

Qy        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
              |||||||||||||||||||||||||||||
Db        995 GGGCTGGCCTATGCTGAGATTGCCAGG------------------------------- 1021

Qy        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
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Db       1022 ----------------------------------------CTTTGTGGTGCTGGCTTC 1039

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Db       1160 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 1219

Qy        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
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Qy        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
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Job time : 471 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 9, 2003, 09:54:13 ; Search time 504 Seconds
(without alignments)
6485.159 Million cell updates/sec

Title: US-09-869-414A-3
Perfect score: 2070
Sequence: 1 atggcccaagccctgccctg.....aaaaaaaaaaaaaaaaaaaa 2070

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1105431 seqs, 789497651 residues

Total number of hits satisfying chosen parameters: 2210862

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2070	100.0	2070	9	US-09-869-414-3	Sequence 3, Appli
2	2070	100.0	2070	9	US-09-548-366-3	Sequence 3, Appli
3	2070	100.0	2070	10	US-09-794-927-3	Sequence 3, Appli
4	2070	100.0	2070	10	US-09-795-847-3	Sequence 3, Appli
5	2070	100.0	2070	10	US-09-794-743-3	Sequence 3, Appli
6	2070	100.0	2070	10	US-09-794-748-3	Sequence 3, Appli
7	2070	100.0	2070	10	US-09-794-925-3	Sequence 3, Appli
8	2070	100.0	2070	10	US-09-681-442-3	Sequence 3, Appli
9	2032	98.2	2541	9	US-09-969-671A-1	Sequence 1, Appli
10	2032	98.2	2541	9	US-10-308-365-1	Sequence 1, Appli
11	2010	97.1	3252	9	US-09-795-903A-1	Sequence 1, Appli
12	2010	97.1	3252	9	US-10-032-818-1	Sequence 1, Appli
13	2010	97.1	3252	10	US-09-796-264-1	Sequence 1, Appli
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16	1887.2	91.2	1977	9	US-09-548-366-5	Sequence 5, Appli
17	1887.2	91.2	1977	10	US-09-794-927-5	Sequence 5, Appli
18	1887.2	91.2	1977	10	US-09-795-847-5	Sequence 5, Appli
19	1887.2	91.2	1977	10	US-09-794-743-5	Sequence 5, Appli
20	1887.2	91.2	1977	10	US-09-794-748-5	Sequence 5, Appli
21	1887.2	91.2	1977	10	US-09-794-925-5	Sequence 5, Appli
22	1887.2	91.2	1977	10	US-09-681-442-5	Sequence 5, Appli
23	1843.4	89.1	2370	9	US-09-969-671A-3	Sequence 3, Appli
24	1843.4	89.1	2370	9	US-10-308-365-3	Sequence 3, Appli
25	1655.8	80.0	1746	9	US-09-924-340-23	Sequence 23, Appl
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37	1504.4	72.7	1506	9	US-10-214-932-103	Sequence 103, App
38	1487.4	71.9	1911	9	US-09-470-954A-44	Sequence 44, Appl
39	1487	71.8	1542	9	US-10-322-684-1	Sequence 1, Appli
40	1395.4	67.4	2158	10	US-09-917-800A-1665	Sequence 1665, Ap
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43	1359	65.7	1362	10	US-09-794-927-29	Sequence 29, Appl
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ALIGNMENTS

RESULT 1
US-09-869-414-3
; Sequence 3, Application US/09869414
; Publication No. US20030077226A1
; GENERAL INFORMATION:
; APPLICANT: Beinkowski et al.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND US
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280M
; CURRENT APPLICATION NUMBER: US/09/869,414
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-869-414-3

Query Match 100.0%; Score 2070; DB 9; Length 2070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Publication No. US20030104365A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES THEREFOR
; FILE REFERENCE: 28341/6280A
; CURRENT APPLICATION NUMBER: US/09/548,366

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;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  65
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 2070
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-548-366-3

  Query Match           100.0%;  Score 2070;  DB 9;  Length 2070;
  Best Local Similarity  100.0%;  Pred. No. 0;
Matches 2070;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120

Qy        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy        241 GTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300

Qy        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
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Db        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
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Db        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
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Db        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540

Qy        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
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Db        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600

Qy        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
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Db        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660

Qy        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
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Db        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720

Qy        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
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Db        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780

Qy        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
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Db        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840

Qy        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
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Db        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900

Qy        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
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Db        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960

Qy        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
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Db        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020

Qy       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
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Db       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080

Qy       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
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Db       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140

Qy       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
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Db       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200

Qy       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260

Qy       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320

Qy       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380

Qy       1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440

Qy       1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500

Qy       1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560

Qy       1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620

Qy       1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680

Qy       1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740

Qy       1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800

Qy       1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860

Qy       1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
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Db       1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920

Qy       1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
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Db       1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980

Qy       1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040

Qy       2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
             ||||||||||||||||||||||||||||||
Db       2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070


RESULT 3
US-09-794-927-3
; Sequence 3, Application US/09794927
; Patent No. US20010016324A1
  GENERAL INFORMATION:
   APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280FG
;  CURRENT APPLICATION NUMBER: US/09/794,927
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 2070
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-794-927-3

  Query Match           100.0%;  Score 2070;  DB 10;  Length 2070;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2070;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120

Qy        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
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Db        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
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Db        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
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Db        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300

Qy        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
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Db        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
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Db        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
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Db        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
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Db        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540

Qy        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
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Qy        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
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Qy        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
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Db        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720

Qy        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
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Db        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780

Qy        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840

Qy        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
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Db        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900

Qy        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
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Db        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960

Qy        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
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Qy       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
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Qy       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
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Qy       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
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Db       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260

Qy       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320
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Qy       1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440
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Db       1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440

Qy       1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500

Qy       1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
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Db       1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560

Qy       1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620
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Qy       1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680
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Db       1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680

             1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740
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Db       1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740

Qy       1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
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Db       1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800

Qy       1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
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Db       1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860

Qy       1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
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Db       1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920

Qy       1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
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Db       1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980

Qy       1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040

Qy       2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
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Db       2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
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RESULT 4
US-09-795-847-3
; Sequence 3, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-795-847-3

Query Match 100.0%; Score 2070; DB 10; Length 2070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
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Db         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120

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Db        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
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Db        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy        241 GTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
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Qy        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
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Db        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
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Db        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

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Db        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

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Db       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140

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Db       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320

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Db       1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560

Qy       1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620
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             1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680
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Qy       1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740

Qy       1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
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Db       1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800

Qy       1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
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RESULT 5
US-09-794-743-3
; Sequence 3, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-794-743-3

Query Match 100.0%; Score 2070; DB 10; Length 2070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
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Qy        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
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Db        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780

Qy        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
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Qy        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
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Db       2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
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RESULT 6
US-09-794-748-3
; Sequence 3, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280JL
; CURRENT APPLICATION NUMBER: US/09/794,748
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2070
; TYPE: DNA

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;   ORGANISM: Homo sapiens
US-09-794-748-3

  Query Match           100.0%;  Score 2070;  DB 10;  Length 2070;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2070;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120

Qy        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy        241 GTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300

Qy        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
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Db        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
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Db        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
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Db        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540

Qy        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
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Db        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600

Qy        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
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Db        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660

Qy        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720

Qy        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
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Db        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780

Qy        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840

Qy        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
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Db        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900

Qy        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
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Db        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960

Qy        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
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Qy       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
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Qy       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
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Db       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140

Qy       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
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Db       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260

Qy       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320

Qy       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
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Db       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380

Qy       1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440

Qy       1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560

Qy       1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620

Qy       1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680
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Db       1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680

Qy       1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740

Qy       1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
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Db       1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800

Qy       1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860

Qy       1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
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Db       1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920

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Db       1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980

Qy       1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
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Db       1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040

Qy       2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
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Db       2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
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RESULT 7
US-09-794-925-3
; Sequence 3, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280HI
;  CURRENT APPLICATION NUMBER: US/09/794,925
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
   PRIOR APPLICATION NUMBER:  60/155,493
   PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 2070
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-794-925-3

  Query Match           100.0%;  Score 2070;  DB 10;  Length 2070;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2070;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
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Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120

Qy        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
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Db        121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
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Db        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
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Db        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300

Qy        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
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Db        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
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Qy        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
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Db        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600

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Qy        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
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Db        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720

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Db        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780

Qy        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
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Db        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840

Qy        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
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Db        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900

Qy        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
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Db        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960

Qy        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
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Qy       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
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Db       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080

Qy       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
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Qy       1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
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Db       1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560

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Db       1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620
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Qy       1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680
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Db       1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680

Qy       1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740
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Db       1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740

Qy       1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
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Db       1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800

Qy       1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
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Db       1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860

Qy       1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
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Db       1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920

Qy       1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
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Db       1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980

Qy       1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
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Db       1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040

Qy       2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
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Db       2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
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RESULT 8
US-09-681-442-3
; Sequence 3, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/681,442
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/416,901
, PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-681-442-3

Query Match 100.0%; Score 2070; DB 10; Length 2070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
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Db          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120

Qy        121 CTGCGGCTGCCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGCGGCTGCCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy        241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
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Qy        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
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Db        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
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Db        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
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Db        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
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Qy        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
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Db        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660

Qy        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
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Db        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840

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Db        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900

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Qy        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
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Qy       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320
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Qy       1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620
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Db       1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800

Qy       1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
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Qy       2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
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Db       2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
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RESULT 9
US-09-969-671A-1
; Sequence 1, Application US/09969671A
; Publication No. US20030036112A1
; GENERAL INFORMATION:
; APPLICANT: CHAPMAN, CONRAD G.
; APPLICANT: MURPHY, KAY
; APPLICANT: POWELL, DAVID J.
; APPLICANT: SMITH, TRUDI S.
; TITLE OF INVENTION: ASP2
; FILE REFERENCE: GH-70368-D1
; CURRENT APPLICATION NUMBER: US/09/969,671A
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: UK 9701684.4
; PRIOR FILING DATE: 1997-01-28
; PRIOR APPLICATION NUMBER: 09/009,191
; PRIOR FILING DATE: 1998-01-20
; PRIOR APPLICATION NUMBER: 09/694,200
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2541
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unknown
; LOCATION: (2455)(2456)(2463)(2478)(2480)(2497)(2507)(2509)(2512)(2516)
; LOCATION: (2520)(2522)(2525)(2529)(2539)(2540)
; OTHER INFORMATION: Wherein n can be represented by a, c, t, or g
US-09-969-671A-1

Query Match 98.2%; Score 2032; DB 9; Length 2541;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2049; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

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Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
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Qy        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
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Qy        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
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Qy       661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
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Db       721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780

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Db       781 GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840

Qy       841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
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Db       841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900

Qy       901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
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            961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
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Qy      1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
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Qy      1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
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Qy      1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
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Qy      1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
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Db      1621 CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCA 1680

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Qy      1800 TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGA 1859
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Qy      1980 TTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTG 2039
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Db      1981 TTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTG 2040

Qy      2040 AATTAAAAAAAAAAAAAAAA 2059
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Db      2041 AATTAAAAAAAAAAACTAGA 2060
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RESULT 10
US-10-308-365-1
; Sequence 1, Application US/10308365
; Publication No. US20030109022A1
; GENERAL INFORMATION:
;  APPLICANT: CHAPMAN, CONRAD G.
;  APPLICANT:  MURPHY, KAY
;  APPLICANT:  POWELL, DAVID J.
;  APPLICANT:  SMITH, TRUDI S.
;  TITLE OF INVENTION: ASP 2
;  FILE REFERENCE: GH-70368-2
;  CURRENT APPLICATION NUMBER: US/10/308,365
;  CURRENT FILING DATE:  2002-12-03
;  PRIOR APPLICATION NUMBER: US/09/694,200
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: UK 9701684.4
;  PRIOR FILING DATE: 1997-01-28
;  PRIOR APPLICATION NUMBER: 09/009,191
;  PRIOR FILING DATE: 1998-01-20
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 2541
;   TYPE: DNA
;   ORGANISM: HOMO SAPIENS
;   FEATURE: FEATURE: MISCELLANEOUS FEATURE
;   NAME/KEY: UNSURE
;   LOCATION: (2455)(2456)(2463)(2478)(2480)(2497)(2507)(2509)(2512)(2516)(2520)
;   LOCATION: (2522)(2525)(2529)(2539)(2540)
;   OTHER INFORMATION: OTHER INFORMATION: n= a, g, c or t
US-10-308-365-1

  Query Match           98.2%;  Score 2032;  DB 9;  Length 2541;
  Best Local Similarity   99.5%;  Pred. No. 0;
  Matches 2049;  Conservative    0;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120

Qy        121 CTGCGGCTGCCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGCGGCTGCCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
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Db        181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
Qy        241 GTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
Db        241 GTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
Qy        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
Db        301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
Qy        361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
Db        361 TACCGGGACCTCCGGAAGGGTGTGTATGAGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
Qy        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
Db        421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
          481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
Db        481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
Qy        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
Db        541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
Qy        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
Db        601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGCTTC 660
Qy        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
Db        661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
Qy        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
Db        721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
Qy        781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
Db        781 GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
Qy        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
Db        841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
          901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
Db        901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
Qy        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
Db        961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
Qy       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
Db       1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
Qy       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
Db       1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
Qy       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
Db       1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
Qy       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
Db       1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
Qy       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320
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Db       1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320
Qy       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
Db       1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
Qy       1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440
Db       1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440
Qy       1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
Db       1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
Qy       1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT-GGACCACACCTCCGTGGTTC 1559
Db       1501 AAGTGAGGAGGCCCATGGGAGAAAGATAGAGATTCCCCTGGGACCACACCTCCGTGGTTC 1560
Qy       1560 ACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTC 1619
Db       1561 ACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTC 1620
Qy       1620 CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCA 1679
Db       1621 CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCA 1680
Qy       1680 GGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATAC 1739
Db       1681 GGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATAC 1740
Qy       1740 TCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACC 1799
Db       1741 TCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACC 1800
Qy       1800 TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGA 1859
Db       1801 TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGA 1860
Qy       1860 AGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAA 1919
Db       1861 AGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCGGGCAGAGAA 1920
Qy       1920 GAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTAT 1979
Db       1921 GAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTAT 1980
Qy       1980 TTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTG 2039
Db       1981 TTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTG 2040
Qy       2040 AATTAAAAAAAAAAAAAAAA 2059
Db       2041 AATTAAAAAAAAAAACTAGA 2060
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RESULT 11
US-09-795-903A-1
; Sequence 1, Application US/09795903A
; Patent No. US20020164760A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; TITLE OF INVENTION: of Use Thereof
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/795,903A
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604,608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836

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;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: 60/178,368
;  PRIOR FILING DATE: 2000-01-27
;  PRIOR APPLICATION NUMBER: 60/210,292
;  PRIOR FILING DATE: 2000-06-08
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 3252
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-795-903A-1

  Query Match             97.1%;  Score 2010;  DB 9;  Length 3252;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 2013;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         40 GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC  99
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           1 GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC  60

         100 CTGGGGGGCGCCCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAG 159
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 CTGGGGGGCGCCCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAG 120

Qy        160 CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 180

Qy        220 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 279
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 240

Qy        280 ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTAC 339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTAC 300

Qy        340 CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC 399
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC 360

Qy        400 CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC 459
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC 420

Qy        460 GTCACTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC 519
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTCACTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC 480

          520 TCCAACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC 579
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Db        481 TCCAACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC 540

Qy        580 CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG 639
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG 600

Qy        640 CACCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGG 699
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGG 660

Qy        700 AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC 759
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC 720

Qy        760 ATCCGGCGGGAGTGGTATTATGAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGAT 819
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        721 ATCCGGCGGGAGTGGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGAT 780

Qy        820 CTGAAAATGGACTGCAAGGAGTACAACTATGACAAGAGCATTGTGGACAGTGGCACCACC 879
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Db        781 CTGAAAATGGACTGCAAGGAGTACAACTATGACAAGAGCATTGTGGACAGTGGCACCACC 840

Qy        880 AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC 939
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC 900

Qy        940 TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA 999
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA 960

Qy       1000 GGCACCACCCCTTGGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC 1059
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GGCACCACCCCTTGGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC 1020

Qy       1060 AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG 1119
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG 1080

Qy       1120 GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT 1179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT 1140

Qy       1180 ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT 1239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT 1200

Qy       1240 GGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC 1299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC 1260

Qy       1300 CCTTTTGTCACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA 1359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CCTTTTGTCACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA 1320

Qy       1360 ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC 1419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC 1380

Qy       1420 TGCCTCATGGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT 1479
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TGCCTCATGGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT 1440

Qy       1480 GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT 1539
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT 1500

Qy       1540 GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC 1599
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC 1560

Qy       1600 CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA 1659
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA 1620

Qy       1660 GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG 1719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG 1680

Qy       1720 CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT 1779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT 1740

Qy       1780 TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATT 1839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATT 1800

Qy       1840 CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCC 1899
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Db       1801 CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCC 1860

Qy       1900 TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA 1959
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Db       1861 TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA 1920

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Qy       2020 GGTGCAAAGATTGCCTCTTGAATTAAAAAAAAAAAAAA 2057
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Db       1981 GGTGCAAAGATTGCCTCTTGAATTAAAAAAAAACTAGA 2018


RESULT 12
US-10-032-818-1
; Sequence 1, Application US/10032818
; Publication No. US20030092629A1
; GENERAL INFORMATION:
;  APPLICANT: Tang, Jordan J.N.
;  APPLICANT:  Koelsch, Gerald
;  APPLICANT:  Ghosh, Arun K.
;  TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
;  FILE REFERENCE: 2932.1006-007
;  CURRENT APPLICATION NUMBER: US/10/032,818
   CURRENT FILING DATE:  2001-12-28
   PRIOR APPLICATION NUMBER: US 60/275,756
   PRIOR FILING DATE: 2001-03-14
;  PRIOR APPLICATION NUMBER: US 60/258,705
;  PRIOR FILING DATE: 2000-12-28
;  NUMBER OF SEQ ID NOS: 83
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 3252
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-032-818-1

  Query Match             97.1%;  Score 2010;  DB 9;  Length 3252;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 2013;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          40 GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC 99
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Db           1 GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC 60

Qy         100 CTGGGGGGCGCCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAG 159
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 CTGGGGGGCGCCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAG 120

Qy         160 CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 219
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Db         121 CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 180

           220 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 279
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Db         181 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 240

Qy         280 ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTAC 339
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Db         241 ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTAC 300

Qy         340 CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC 399
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Db         301 CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC 360

Qy         400 CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC 459
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Db         361 CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC 420

Qy         460 GTCACTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC 519
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 GTCACTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC 480

Qy         520 TCCAACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC 579
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 TCCAACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC 540

Qy         580 CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG 639
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Db         541 CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG 600

Qy         640 CACCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGG 699
                 || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 CAGCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGG 660

Qy         700 AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC 759
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC 720

Qy         760 ATCCGGCGGGAGTGGTATTATGAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGAT 819
                 |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db         721 ATCCGGCGGGAGTGGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGAT 780

Qy         820 CTGAAAATGGACTGCAAGGAGTACAACTATGACAAGAGCATTGTGGACAGTGGCACCACC 879
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 CTGAAAATGGACTGCAAGGAGTACAACTATGACAAGAGCATTGTGGACAGTGGCACCACC 840

Qy         880 AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC 939
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC 900

Qy         940 TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA 999
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA 960

Qy        1000 GGCACCACCCCTTGGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC 1059
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 GGCACCACCCCTTGGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC 1020

Qy        1060 AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG 1119
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG 1080

Qy        1120 GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT 1179
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1081 GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT 1140

Qy        1180 ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT 1239
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1141 ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT 1200

Qy        1240 GGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC 1299
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1201 GGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC 1260

Qy        1300 CCTTTTGTCACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA 1359
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1261 CCTTTTGTCACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA 1320

Qy        1360 ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC 1419
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1321 ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC 1380

Qy        1420 TGCCTCATGGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT 1479
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1381 TGCCTCATGGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT 1440

Qy        1480 GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT 1539
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1441 GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT 1500

Qy        1540 GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC 1599
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1501 GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC 1560

Qy        1600 CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA 1659
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1561 CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA 1620

Qy        1660 GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG 1719
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1621 GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG 1680

Qy       1720 CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT 1779
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT 1740

Qy       1780 TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATT 1839
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATT 1800

Qy       1840 CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCC 1899
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCC 1860

Qy       1900 TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA 1959
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA 1920

Qy       1960 GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT 2019
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         1921 GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT 1980

Qy       2020 GGTGCAAAGATTGCCTCTTGAATTAAAAAAAAAAAAAA 2057
             |||||||||||||||||||||||||||||||||  | |
Db       1981 GGTGCAAAGATTGCCTCTTGAATTAAAAAAAAACTAGA 2018


RESULT 13
US-09-796-264-1
; Sequence 1, Application US/09796264
; Patent No. US20020049303A1
; GENERAL INFORMATION:
;  APPLICANT: Tang, Jordan J.N.
;  APPLICANT:  Lin, Xinli
;  APPLICANT:  Koelsch, Gerald
;  TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
;  TITLE OF INVENTION:  of Use Thereof
;  FILE REFERENCE: OMRF 179
;  CURRENT APPLICATION NUMBER: US/09/796,264
;  CURRENT FILING DATE:  2001-02-28
;  PRIOR APPLICATION NUMBER: 09/604,608
;  PRIOR FILING DATE: 2000-06-27
;  PRIOR APPLICATION NUMBER: 60/168,060
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: 60/177,836
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: 60/178,368
;  PRIOR FILING DATE: 2000-01-27
;  PRIOR APPLICATION NUMBER: 60/210,292
;  PRIOR FILING DATE: 2000-06-08
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 3252
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-796-264-1

  Query Match             97.1%;  Score 2010;  DB 10;  Length 3252;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 2013;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         40 GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC 99
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC 60

Qy        100 CTGGGGGGCGCCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAG 159
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTGGGGGGCGCCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAG 120

Qy        160 CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 180

Qy        220 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 279
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 240

Qy        280 ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTAC 339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTAC 300

Qy        340 CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC 399
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC 360

Qy        400 CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC 459
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC 420

Qy        460 GTCACTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC 519
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTCACTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC 480

Qy        520 TCCAACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC 579
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC 540

Qy        580 CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG 639
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG 600

Qy        640 CACCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGG 699
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGG 660

Qy        700 AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC 759
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC 720

Qy        760 ATCCGGCGGGAGTGGTATTATGAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGAT 819
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        721 ATCCGGCGGGAGTGGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGAT 780

Qy        820 CTGAAAATGGACTGCAAGGAGTACAACTATGACAAGAGCATTGTGGACAGTGGCACCACC 879
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CTGAAAATGGACTGCAAGGAGTACAACTATGACAAGAGCATTGTGGACAGTGGCACCACC 840

Qy        880 AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC 939
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC 900

Qy        940 TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA 999
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Db        901 TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA 960

Qy       1000 GGCACCACCCCTTGGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC 1059
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GGCACCACCCCTTGGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC 1020

Qy       1060 AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG 1119
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG 1080

Qy       1120 GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT 1179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT 1140

Qy       1180 ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT 1239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT 1200

Qy       1240 GGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC 1299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC 1260
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Qy       1300 CCTTTTGTCACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA 1359
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Db       1261 CCTTTTGTCACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA 1320

Qy       1360 ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC 1419
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC 1380

Qy       1420 TGCCTCATGGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT 1479
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TGCCTCATGGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT 1440

Qy       1480 GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT 1539
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT 1500

Qy       1540 GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC 1599
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC 1560

         1600 CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA 1659
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA 1620

Qy       1660 GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG 1719
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG 1680

Qy       1720 CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT 1779
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT 1740

Qy       1780 TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATT 1839
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATT 1800

Qy       1840 CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCC 1899
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCC 1860

Qy       1900 TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA 1959
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA 1920

Qy       1960 GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT 2019
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Db       1921 GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT 1980

         2020 GGTGCAAAGATTGCCTCTTGAATTAAAAAAAAAAAAAA 2057
             ||||||||||||||||||||||||||||||||  | |
Db       1981 GGTGCAAAGATTGCCTCTTGAATTAAAAAAAAACTAGA 2018
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RESULT 14
US-09-845-226-1
; Sequence 1, Application US/09845226
; Patent No. US20020115600A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Hong, Lin
; APPLICANT: Ghosh, Arun K.
; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
; FILE REFERENCE: OMRF 182
; CURRENT APPLICATION NUMBER: US/09/845,226
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 09/603,713
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3252
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-845-226-1

Query Match 97.1%; Score 2010; DB 10; Length 3252;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2013; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy         40 GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC 99
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC 60

Qy        100 CTGGGGGGCGCCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAG 159
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTGGGGGGCGCCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAG 120

Qy        160 CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 180

Qy        220 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 279
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGAT 240

Qy        280 ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTAC 339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTAC 300

Qy        340 CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC 399
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC 360

Qy        400 CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC 459
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC 420

Qy        460 GTCACTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC 519
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTCACTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC 480

Qy        520 TCCAACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC 579
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC 540

Qy        580 CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG 639
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG 600

Qy        640 CACCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGG 699
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGG 660

Qy        700 AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC 759
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC 720

Qy        760 ATCCGGCGGGAGTGGTATTATGAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGAT 819
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        721 ATCCGGCGGGAGTGGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGAT 780

Qy        820 CTGAAAATGGACTGCAAGGAGTACAACTATGACAAGAGCATTGTGGACAGTGGCACCACC 879
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CTGAAAATGGACTGCAAGGAGTACAACTATGACAAGAGCATTGTGGACAGTGGCACCACC 840

Qy        880 AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC 939
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC 900
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Qy       940 TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA 999
Db       901 TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA 960

Qy      1000 GGCACCACCCCTTGGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC 1059
Db       961 GGCACCACCCCTTGGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC 1020

Qy      1060 AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG 1119
Db       1021 AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG 1080

Qy      1120 GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT 1179
Db       1081 GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT 1140

Qy      1180 ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT 1239
         1141 ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT 1200

         1240 GGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC 1299
Db       1201 GGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC 1260

Qy      1300 CCTTTTGTCACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA 1359
Db       1261 CCTTTTGTCACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA 1320

Qy      1360 ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC 1419
Db       1321 ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC 1380

Qy      1420 TGCCTCATGGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT 1479
Db       1381 TGCCTCATGGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT 1440

Qy      1480 GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT 1539
Db       1441 GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT 1500

Qy      1540 GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC 1599
Db       1501 GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC 1560

Qy      1600 CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA 1659
Db       1561 CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA 1620

         1660 GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG 1719
Db       1621 GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG 1680

Qy      1720 CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT 1779
Db       1681 CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT 1740

Qy      1780 TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATT 1839
Db       1741 TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATT 1800

Qy      1840 CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCC 1899
Db       1801 CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCC 1860

Qy      1900 TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA 1959
Db       1861 TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA 1920

Qy      1960 GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT 2019
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Qy      2020 GGTGCAAAGATTGCCTCTTGAATTAAAAAAAAAAAAAA 2057
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RESULT 15
US-09-869-414-5
; Sequence 5, Application US/09869414
; Publication No. US20030077226A1
; GENERAL INFORMATION:
; APPLICANT: Beinkowski et al.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND US
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280M
; CURRENT APPLICATION NUMBER: US/09/869,414
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1977
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-869-414-5

Query Match 91.2%; Score 1887.2; DB 9; Length 1977;
Best Local Similarity 96.2%; Pred. No. 0;
Matches 1974; Conservative 0; Mismatches 3; Indels 75; Gaps 1;

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Qy         1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
Db         1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy        61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
Db        61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120

Qy       121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
Db       121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy       181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
Db       181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy       241 GTGGGCAGCCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
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Qy       301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
Db       301 GTGGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy       361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
Db       361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy       421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
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Qy       481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
Db       481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
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Qy       541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
            ||||||||||||||||||||||||||
Db       541 GGGCTGGCCTATGCTGAGATTGCCAGG------------------------------- 567

Qy       601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
                                                  ||||||||||||||||||
Db       568 ----------------------------------------CTTTGTGGTGCTGGCTTC 585

Qy       661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       586 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 645

Qy       721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       646 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 705

Qy       781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
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Db       706 GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 765

Qy       841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
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Db       766 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 825

Qy       901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
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Db       826 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 885

Qy       961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       886 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 945

Qy      1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
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Db       946 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1005

Qy      1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1006 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1065

Qy      1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
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Db      1066 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1125

Qy      1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1126 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1185

Qy      1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1186 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1245

Qy      1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
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Db      1246 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1305

Qy      1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1306 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1365

Qy      1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
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Db      1366 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1425

Qy      1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
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Db      1426 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1485

Qy      1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620
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Qy      1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG 1680
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Qy      1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740
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Db      1606 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1665

Qy      1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
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Db      1666 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1725

Qy      1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
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Db      1726 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1785

Qy      1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
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Db      1786 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1845

Qy      1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
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Search completed: July 9, 2003, 14:19:07
Job time : 507 secs